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OM nucleic - nucleic search, using sw model

Run on: April 28, 2005, 16:13:19 ; Search time 675 Seconds
(without alignments)
9190.947 Million cell updates/sec

Title: US-10-688-011-1
Perfect score: 1048
Sequence: 1 attgcttctgttagatga.....agtcataataaaaaaaaa 1048

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1048	100.0	1048	3	AAA12616	Aaa12616 cDNA enco
2	441	42.1	1050	2	AAQ71520	Aaq71520 Hornet ph
3	426.2	40.7	1341	2	AAQ71523	Aaq71523 Yellowjac
4	49.2	4.7	460	8	ABX47675	Abx47675 Bovine ES
5	49	4.7	1301	4	ABL06057	Ab106057 Drosophil
6	49	4.7	4016	4	ABL06056	Ab106056 Drosophil
7	47.4	4.5	4590	5	AAH24065	Aah24065 Yeast AOD
8	47.2	4.5	1584	12	ADP28939	Adp28939 Human sec
9	47	4.5	3564	13	ADQ38815	Adq38815 Human SNP
10	46.8	4.5	1526	6	ABL60540	Ab160540 Human lip
11	46.8	4.5	3635	9	ACH03823	Ach03823 Human cDN
12	46.2	4.4	13326	6	ABL33713	Ab133713 Human imm
13	45.8	4.4	2000	8	ADA71938	Ada71938 Rice gene
14	45.8	4.4	7786	6	ABA92788	Ab92788 Buchnera
15	45.6	4.4	1383	10	ADI23669	Adi23669 Mouse LPD
16	45.6	4.4	1605	6	ABK63642	Abk63642 Rat seque
17	45.6	4.4	1605	10	ADB52543	Adb52543 Primary x
18	45.6	4.4	1639	10	ADB57969	Adb57969 Toxicity-
19	45.6	4.4	2056	10	ADI23667	Adi23667 Mouse LPD
20	45.2	4.3	1383	6	AAD27797	Aad27797 Human pan

21	45.2	4.3	1404	6	AB159436	Ab159436 Nucleotid
22	45.2	4.3	1422	6	ABN87363	Abn87363 Human lip
23	45.2	4.3	1428	13	ADQ89959	Adq89959 Antagonis
24	45.2	4.3	1540	6	ABN60002	Abn60002 Novel hum
25	45.2	4.3	2352	4	AAD03848	Aad03848 Human lip
26	45.2	4.3	3549	2	AAV41319	Aav41319 Human lip
27	45.2	4.3	3549	2	AAZ32183	Aaz32183 Human lip
28	45.2	4.3	3549	6	ABL66907	Ab166907 Lung canc
29	45.2	4.3	3549	6	ABT10903	Abt10903 Human bre
30	45.2	4.3	3549	6	ABT13006	Abt13006 Human lip
31	45.2	4.3	3549	12	ADM41259	Adm41259 Human lip
32	45.2	4.3	3549	13	ADR14098	Adr14098 Human NF-
33	45.2	4.3	3549	13	ADP23567	Adp23567 PRO polyp
34	45.2	4.3	3549	13	ADR73479	Adr73479 Human lip
35	45.2	4.3	4075	10	ADB47407	Adb47407 Human cDN
36	45.2	4.3	4314	12	ADQ23742	Adq23742 Human sof
37	45	4.3	3185	6	AAI72633	Aai72633 Human 232
38	44.6	4.3	17294	6	ABL32987	Ab132987 Human imm
39	44.4	4.2	421	8	ABX42958	Abx42958 Bovine ES
40	44.4	4.2	453	8	ABX36741	Abx36741 Bovine ES
41	44.4	4.2	938	5	AAD07722	Aad07722 Human sec
42	44.4	4.2	1603	6	ABT13009	Abt13009 Human hep
43	44.4	4.2	1603	10	ADD29786	Add29786 Human tuc
44	44.2	4.2	1767	2	AAx99572	Aax99572 Nucleic a
45	44.2	4.2	8634	6	ABL33056	Ab133056 Human imm

ALIGNMENTS

RESULT 1	
AAA12616	AAA12616 standard; cDNA; 1048 BP.
XX	
AC	AAA12616;
XX	
DT	25-JUL-2000 (first entry)
XX	
DE	cDNA encoding a Pol a venom phospholipase A1 polypeptide.
XX	
KW	Pol a venom; phospholipase A1; paper wasp; immune response; immunogen;
KW	vespid venom; allergen-specific allergy; hymenoptera venom;
KW	autoimmune condition; allergic condition; viral infection; HIV;
KW	human immunodeficiency virus; Herpes Simplex virus; papilloma virus; ss.
OS	Polistes annularis.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..963
FT	/*tag= a
FT	/product= "venom phospholipase A1"
FT	1..54
FT	/*tag= b
FT	55..963
FT	/*tag= c
PN	WO200018896-A1.
XX	
PD	06-APR-2000.
XX	
PF	01-OCT-1999; 99WO-US023211.
XX	
PR	01-OCT-1998; 98US-00166205.
XX	
PA	(UYRQ) UNIV ROCKEFELLER.
XX	
PI	King TP;
XX	
DR	WPI; 2000-293139/25.
DR	P-PSDB; AAY84613.
XX	
PT	New nucleic acids encode enzymes of wasp venom, are useful to treat
PT	insect sting allergy or immune system-related disorders and differ from

PT the genomic sequences in that introns have been removed.

XX Claim 5; Fig 1; 72pp; English.

XX
XX
XX The present sequence encodes a Pol a venom phospholipase A1 polypeptide, isolated from the paper wasp. The enzyme acts on phospholipid substrates, e.g. to hydrolyse fatty acids. The recombinant Polistinae venom is used to modulate an immune response to an immunogen in a mammal, particularly a vespid venom allergen-specific allergy, or allergy to other hymenoptera venom. Alternatively the venom enzyme is used to treat an immunologically affected disease or disorder, particularly a pathogenic disease or disorder, an autoimmune condition, an allergic condition, especially an allergy to hymenoptera venom, or a viral infection, especially human immunodeficiency virus (HIV), Herpes Simplex virus or papilloma virus. The enzyme is also useful to diagnose allergy

XX Sequence 1048 BP; 362 A; 160 C; 210 G; 316 T; 0 U; 0 Other;

Query Match 100.0%; Score 1048; DB 3; Length 1048;
Best Local Similarity 100.0%; Pred. No. 1.3e-232;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTTCTGTTAGATGATTCGACGACATTTGAAATGTAACCTTGATAGAGCATG 60
DB 1 ATTGCTTCTGTTAGATGATTCGACGACATTTGAAATGTAACCTTGATAGAGCATG 60
QY 61 TCTCCGATTTGACTTTTATGAGAAAGATATAGTATCTATGTTTACTCAAGGATAAG 120
DB 61 TCTCCGATTTGACTTTTATGAGAAAGATATAGTATCTATGTTTACTCAAGGATAAG 120
QY 121 CGAGATGGTATTTATTTAAGAAAGAACTTTAAGAAATAGCATCTGTTTACAAGTCT 180
DB 121 CGAGATGGTATTTATTTAAGAAAGAACTTTAAGAAATAGCATCTGTTTACAAGTCT 180
QY 181 ACAATATCAAAACAAGTTGATTTCTTATACATGGTTTCTTCAACTGGCAATATGAA 240
DB 181 ACAATATCAAAACAAGTTGATTTCTTATACATGGTTTCTTCAACTGGCAATATGAA 240
QY 241 AACTTCGTGCTATGTCGAAAGCTTTAATAGAAAAAGATGATTTCTGTAATTCGGTC 300
DB 241 AACTTCGTGCTATGTCGAAAGCTTTAATAGAAAAAGATGATTTCTGTAATTCGGTC 300
QY 301 GACTGGAAGAGGGTGCTTGTAAATGCTTTTGCTTCAACAAAGAGCTTTGGTTATTC 360
DB 301 GACTGGAAGAGGGTGCTTGTAAATGCTTTTGCTTCAACAAAGAGCTTTGGTTATTC 360
QY 361 AAAGCCGTTGAAACACAGTCACGTTGAAAAATTTAGCTGATTTTACAAAACACTT 420
DB 361 AAAGCCGTTGAAACACAGTCACGTTGAAAAATTTAGCTGATTTTACAAAACACTT 420
QY 421 GTAGAAAAATATAAGTGTGATATCAAAATATACGATTGATCGGGCATAGTTGGCGCG 480
DB 421 GTAGAAAAATATAAGTGTGATATCAAAATATACGATTGATCGGGCATAGTTGGCGCG 480
QY 481 CATACTTCAGGTTTGGGGAAAAAGAGTTCAAAAGTTAAATTAGGAAAAATACAAGGAA 540
DB 481 CATACTTCAGGTTTGGGGAAAAAGAGTTCAAAAGTTAAATTAGGAAAAATACAAGGAA 540
QY 541 ATTATCGGGCTTGATCTGCTGACCGGTATTTTCATCGAGTGAAGTCCGGACAGACTT 600
DB 541 ATTATCGGGCTTGATCTGCTGACCGGTATTTTCATCGAGTGAAGTCCGGACAGACTT 600
QY 601 TGCGTAACAGACGAGAAATATGTTCAAGTTATACATCAATCAATATTAAGAGTATAT 660
DB 601 TGCGTAACAGACGAGAAATATGTTCAAGTTATACATCAATCAATATTAAGAGTATAT 660
QY 661 TATAATGTTGTAGCGTTGATTTCTACGTGAATATGAGAAAAATCAACCTGTTGCAAT 720
DB 661 TATAATGTTGTAGCGTTGATTTCTACGTGAATATGAGAAAAATCAACCTGTTGCAAT 720
QY 721 GAACCATCCTGCTCTCATACGAAAGCCGTGAATAATCTGACTGAGTGCATAAACATGAA 780
DB 721 GAACCATCCTGCTCTCTCATACGAAAGCCGTGAATAATCTGACTGAGTGCATAAACATGAA 780

QY 781 TGTGTTTATTTGGAACACCATGGAAGAAATATTTACAGCACTCCAAAACCAATTTCCAG 840
DB 781 TGTGTTTATTTGGAACACCATGGAAGAAATATTTACAGCACTCCAAAACCAATTTCCAG 840
QY 841 TGCAAGAGGAGACACTGTGTTTGGCGTTGGATTGAATGCAAAAGTTATCTCTAGAGGC 900
DB 841 TGCAAGAGGAGACACTGTGTTTGGCGTTGGATTGAATGCAAAAGTTATCTCTAGAGGC 900
QY 901 GCATTTTATGACCCGTTGAAGCAAAATGCACTTATGGCCATTAAGAGGATTAACCTT 960
DB 901 GCATTTTATGACCCGTTGAAGCAAAATGCACTTATGGCCATTAAGAGGATTAACCTT 960
QY 961 TAAATTAAACAAAGTCAATGTACACAAAATGTATCTATTGAATGAATTAATGAAT 1020
DB 961 TAAATTAAACAAAGTCAATGTACACAAAATGTATCTATTGAATGAATTAATGAAT 1020
QY 1021 AAACGACAGTCAAAATTAATAAAAAA 1048
DB 1021 AAACGACAGTCAAAATTAATAAAAAA 1048

RESULT 2
AAQ71520
ID AAQ71520 standard; cDNA; 1050 BP.
XX
AC AAQ71520;
XX
DT 25-MAR-2003 (revised)
DT 26-APR-1995 (first entry)
XX
DE Hornet phospholipase Dol ml, cDNA.
XX
KW Hornet phospholipase; vespid venom enzyme; VV;
KW allergen-specific allergic condition; Dol ml; ss.
XX
OS Dolichovespula maculata.
XX
FH Key Location/Qualifiers
FT CDS 1..951
FT /*tag= a
XX
PN W09420623-A1.
XX
PD 15-SEP-1994.
XX
PF 10-MAR-1994; 94WO-US002629.
XX
PR 11-MAR-1993; 93US-00031400.
PR 11-JAN-1994; 94US-00180209.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI King TP;
XX
DR WPI; 1994-303030/37.
DR P-PSDB; AAR60599.
XX
PT Nucleic acid encoding vespid venom enzymes - used to produce polypeptides for diagnosis and treatment of vespid venom allergen-specific allergic conditions.
XX
PS Claim 7; Fig 1; 93pp; English.
XX
CC AAQ71520 is the cDNA sequence that codes for hornet phospholipase (AAR60599), a vespid venom (VV) enzyme. These enzymes were used to produce highly specific and individualised polypeptides for the diagnosis and the treatment of VV-specific allergic conditions. For therapy, the polypeptides or fragments can be administered by oral, nasal or parenteral routes. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 1050 BP; 366 A; 170 C; 215 G; 299 T; 0 U; 0 Other;

Query Match 42.1%; Score 441; DB 2; Length 1050;
Best Local Similarity 67.0%; Pred. No. 3.7e-92;
Matches 665; Conservative 0; Mismatches 310; Indels 18; Gaps 2;

QY 65 CGGATTGTACTTTTAATGAGAAAGATATAGTATCTATGTTTACTCAAGGATAGCGAG 124
DB 56 CCGTATGTCCTTTAGTATGATACAGTTAAGATGATTTTAAACAAGGAAACCGAA 115
QY 125 ATGGTATTTCTTAAGAAAGAACTTTAACGAATTACGATCTGTTTACAAGTCTACA 184
DB 116 AACATGATTTTATACGCTAGATACATGAACAGCACAAATGAATTTAAGAGTCAATCA 175
QY 185 TATCAAAACAAGTGTATTTCTTATACATGTTTCTTCACTGGGAATATGAAACT 244
DB 176 TAAAACGTCAGTGTATTCATTCAGCATGGTTTACTTCGTCTGCAACCGAAAAAATT 235
QY 245 TCGTGTATGTGCGAAAGCTTTAATAGAAAAAGATGATTTCTGTATTTCCGTCGACT 304
DB 236 TCGTGTATGTGCGAGGCTCTATGCAATACAGTGATTTCTTATATATGATGATTT 295
QY 305 GGAAGAAGGCTGCTGTATATGCTTTGCTTCAACAAAGATGCTTTGGGTATTTCCAAG 364
DB 296 GGGGATGGCTGCTGTACTGATGATAACCAAGGCTGGAAGTATATGTTTATTAAGGCTG 355
QY 365 CCGTTGGAACACACGCTCAGCTTGGAAATTTGTAGCTGATTTTACAACAACTACTGTAG 424
DB 356 CCGTTGGAATACACGCTTAGTGGAAATTTTATCGTATGATCGCAAGAACTTGTAG 415
QY 425 AAAAATATAAGTCTGATATCAAAATATACGATTGATCGGCGATAGTTGGCGCGCAT 484
DB 416 AACATATATAAGTCCGATGACAAATATACGACTGTGGGACACAGTTGGCGCACACA 475
QY 485 CTTCAGGTTTTCGGGAAAGAGTCAAAAGTTAAAAATTAGGAAATACAAAGAAATTA 544
DB 476 TTTCAAGTTTCGACAGCAAAAGAGTCAAGAGTTAAATATAGGAAATTTCTGAATTA 535
QY 545 TCGGCTGATCTGCTGACCGGATTTTTCATCGAGTGACTGTCGACAGACTTTGCG 604
DB 536 TTGGGCTGATCTGCTGCGGCTGATTTCAAGAAAAATGATTTGTTCCGAGAGATCTGCG 595
QY 605 TAACAGACCGAATATGTTCAAGTTATACATACATCAATCATATTAGAGTATATTATA 664
DB 596 AGACAGACCGACATTTATGACAAATTTTACATACATCGACCAATTTAGGAACAGAGAA 655
QY 665 ATGTTGTAAGCTGATTTCTACGTAATTTAGGAAAAATCAACCTGTTGC----- 717
DB 656 CTCTTGGACCGTCGATTTCTACATAAATAACGGAAGTATCAACCCGTTGCAGATATA 715
QY 718 --AATGAACATCTGCTCTCATACGAAAGCCGTGAATATCTGACTGAGTGAATAAC 775
DB 716 TTATTTGAGAAACTTGCTCTCATACGAGACCGGAAATACTTTACCGAGTGCATAAGAC 775
QY 776 ATGAATGTTTAAATTGGAACCATGGAAGAATATTTCAGCACCTCCAAACCAATTT 835
DB 776 GCGAATGTTTAAATTGCGGTC-----GCAGTCCAAGATCCGACGCTGTTT 826
QY 836 CCCAGTCAGAGAGACACCTGTGTTTCCGTTGGATTGAATGCAAAAAAGTTATCTGCTA 895
DB 827 CGAAGTCACAAAGAAACGAGTGGCTTTGCGTTGGATTAAACGCAAAAGAAATATCTTAAA 886
QY 896 GAGGCGCATTTTATGACCCGTTGAAGCAAAATGACACCTTATGGCATTAACGAGGGATTA 955
DB 887 GGGGCTCATTTTATGTACCGGTTGAAGCTGAAGCTCCATATTTGCAATTAACACGGAATA 946
QY 956 AACTTTAATTATTAACAAAGTCAATGATACACAAAAATGATATCTATGATGAATATTA 1015
DB 947 TAAATTAATTATTAACAAAAACATTAATGACACAAAGTGCATTTGTTAATGATGAA 1006
QY 1016 TGAATTAACGAACAGTCAAAATTAACAAAAA 1048
DB 1007 TGAATTAATTAAGATTCAAGAAAAA 1039

RESULT 3
AAQ71523
ID AAQ71523 standard; cDNA; 1341 BP.

XX AAQ71523;
AC XX
DT 25-MAR-2003 (revised)
DT 26-APR-1995 (first entry)
XX
DE Yellowjacket phospholipase cDNA.
XX
KM Yellowjacket phospholipase; vespid venom enzyme; VV;
KM allergen-specific allergic condition; ss.
XX
OS Vesputia maculifrons.

FH Key location/Qualifiers
FT CDS 153..1052
FT /*tag= a

PN WO9420623-A1.
XX
PD 15-SEP-1994.
XX

PF 10-MAR-1994; 94WO-US002629.
XX
PR 11-MAR-1993; 93US-00031400.
PR 11-JAN-1994; 94US-00180209.
XX

PA (UVRQ) UNIV ROCKEFELLER.
XX
PI King TP;
XX

DR WPI; 1994-303030/37.
DR P-PSDB; AAR60603.
XX

PT Nucleic acid encoding vespid venom enzymes - used to produce polypeptides
PT for diagnosis and treatment of vespid venom allergen-specific allergic
PT conditions.

PS Claim 6; Fig 5; 93pp; English.
XX

CC AAQ71523 is the cDNA sequence that codes for yellowjacket phospholipase
CC (AAR60603), a vespid venom (VV) enzyme. These enzymes were used to
CC produce highly specific and individualised polypeptides for the diagnosis
CC and the treatment of VV-specific allergen specific conditions. For
CC therapy, the polypeptides or fragments can be administered by oral, nasal
CC or parenteral routes. (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 1341 BP; 473 A; 206 C; 239 G; 423 T; 0 U; 0 Other;

Query Match 40.7%; Score 426.2; DB 2; Length 1341;
Best Local Similarity 66.9%; Pred. No. 1.1e-88;
Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;

QY 64 CCGATTGTACTTTTAATGAGAAAGATATAGTATCTATGTTTACTCAAGGATTAAGCGA 123
DB 156 CCCAATGTCCTTTTAATCTGATACAGTTTGCATTAATTTGAAACAAAGGAAACCGA 215
QY 124 GATGTTATTTCTTAAGAAAGAACTTTAACGAATTACGATCTGTTTACAAGTCTACA 183
DB 216 AATCGTATCTTTATACACTACAGACATTTACGAATCATCTGAATTTAAGAAAAACT 275
QY 184 ATATCAAAACAAGTGTATTTCTTATACATGTTTCTTCACTGGGAATAATGAAC 243
DB 276 ATACACGTCGAGTGTATTCATTTACATATGTTTACTCATCTGCAAGTGAACAAAT 335
QY 244 TTGCTGTATGTCGAAGCTTTAATGAAGAAAGATGATTTCTTGAATTTGCGTGAC 303
DB 336 TTCAATTAATTTAGCAAAAGCTTTGGTAGATTAAGATTAATATATGTTATCTCAATGAT 395
QY 304 TGAAGAAAGGCTGTTGATGCTTTGCTTCAACAAAGATGCTTTGGGTTATTCAAA 363

Db 396 TGGCAGACGGCTGCTTGTACTAATGAAGCTGCAGGTTTAAAGTATTATATATCTCTACT 455
Qy 364 GCCGTTGAAAAACACACGCTCAGCTTGAAAAATTGTAGCTGATTTTACAAACTACTTGTA 423
Db 456 GCTGCTAGAAATACACGTTTGTAGTGGACAATATATCGCTACGATTACCCGAAACTCGTA 515
Qy 424 GAAAAATATAAAGTGTGATATCAAAATATACGATTGATCGGCATAGTTGGCGGCAT 483
Db 516 AAACACTATAAAATCTCGATGGCAATATACGATTAATTGACATAGCTTAGAGACACAT 575
Qy 484 ACTTCAGGTTTTCGGGAAAAGAAGTCAAAAAGTTAAAAATTAGAAAATACAGAATTT 543
Db 576 GCTTCAGGTTTTCGAGGCAAAAAGTTCAAGAGTTAAAAATTAGAAAATATTCTGAATTT 635
Qy 544 ATCGGCTTGATCCTGCTGACCGCTATTTCATCGGAGTGAAGTCTGCCGACAGACTTGC 603
Db 636 ATTGCGCTTGATCCTGCTAGGCTTCTGATTCAAAATCATTGTTCCGAAAAGACTCTGC 695
Qy 604 GTAACAGACGCAATATGTTCAAGTTATACATACATCATATATTAGAGATATTATT 663
Db 696 GAGACAGATGCAGAAATATGTTCAAAATTATACATACATCAAACTATTAGAAACCGAAAA 755
Qy 664 AATGTTGTAGCGCTGATTTCTACGTAATTATGAAAAAATCAACCTGTTGCAATGAA 723
Db 756 ACCCTGTGACCGTGAATTTCTACATGAATAACGGAAGAATCAACCTGTTGCGGTAGA 815
Qy 724 CCATCC-----TGCTCTCATACGAAAGCCGTGAATATCTGACTGATGATATAAA 774
Db 816 TTTTCTCAGAGTTTGTCTCTCATTCGAGAGCCGTGATATACATGCTGATGATATAAA 875
Qy 775 CATGATGTTGTTTAAATGGAACACCATGGAAGAATATTTCAGCAGCTCCAAAAACCAATT 834
Db 876 CACGAATGTTGTTTAAATGGGATACC-----GAAGTCAAGAAGTTCCGACCTATT 926
Qy 835 TCCAGTGCAGAGAGACACCTGTGTTTGGCTTGATGCAATGCAAAAAAGTTATCTGCT 894
Db 927 TCGTGTGCACAAAAACAGAGTGGCTTTCGCTTGATTAACGCAAGAAGTATACTAGT 986
Qy 895 AGAGCGCATTTTATGACCGGTTGAAGCAAAATGCACTTATGCGCATTAAGAGGGGATT 954
Db 987 AGAGCTCATTTTATGACCGGTTGAAGTACTGTTCTTTTGAATTAACAAGGGGAG 1046
Qy 955 AAATTTAATTATTAACAAAGTCAATGTACACAAAATGTATCTATGATGAATATTAA 1014
Db 1047 ATAAATTAATATATAAAAGT-AATTTCCATTCATCGAAATGCAATGTTGTTAATGTGA 1105
Qy 1015 ATGAATAAACGACAGTCAATATAAAA 1041
Db 1106 ATGAATAAATTACCATTTTAACAATAA 1132

RESULT 4
ABX47675
ID ABX47675 standard; cDNA; 460 BP.
XX
AC ABX47675;
XX
DT 21-FEB-2003 (first entry)
XX
DE Bovine EST associated with lactation/muscle/fat deposition #12840.
XX
KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
OS Bos Taurus.
XX
PN US2002137139-A1.
XX
XX 26-SEP-2002.
PD
XX 24-SEP-2001; 2001US-00960352.
PF
XX

PR 12-JAN-1999; 99US-0115707P.
PR 11-JAN-2000; 2000US-00480902.
XX
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX
PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX
DR WPI; 2003-110599/10.
XX
PT New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX
PS Claim 2; SEQ ID NO 12840; 245bp; English.

CC The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non-translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
SQ Sequence 460 BP; 116 A; 107 C; 129 G; 108 T; 0 U; 0 Other;

Query Match 4.7%; Score 49.2; DB 8; Length 460;
Best Local Similarity 51.4%; Pred. No. 0.14;
Matches 148; Conservative 0; Mismatches 128; Indels 12; Gaps 1;

Qy 359 CCAAAGCCGTTGGAACACACGTCACGTTGAAAAATTGTAGCTGATTTTACAAAACCTAC 418
Db 3 CCAAGCGCGGGATATACCAAGCTGTGGGACAGATGTGGCCAAGTTATGAACCTGA 62
Qy 419 TTGTAGAAAAATATAAGTGTGATATCAATATATACGATTGATCGGCGCATAGTTGGGCG 478
Db 63 TGGCGGATGAATTAATATATATCCCTGGGCAATGTGCATCTCTGGGATACAGCCTTGGG 122
Qy 479 CGCATACTTCAGGTTTTCGGGAAAAGAAGTCAAAAAGTTAAAAATTAGAAAATACAGG 538
Db 123 CCCATGCTGCTGTATTTGACGAAGAAGTTCACCAATAAG-----AAGTCAACA 170
Qy 539 AAATTATCGGCTGTATCCTGCTGACCGTATTTTCATCGAGTGAAGTCTCCGACAGAC 598
Db 171 GGATTAACCGCTTAGATCCAGCTGACCTTAACCTTGAGTATGAGAAAGCTCCAAGTGGC 230
Qy 599 TTGCGTAACAGACGAGATATGTTCAAGTTATATACATACATCAATCA 646
Db 231 TTTCTCCTGATGATGCGGATTTTGTAGAGTTTATACACACATTCACCA 278

RESULT 5

ABL06057
ID ABL06057 standard; cDNA; 1301 BP.
XX
AC ABL06057;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 12653.
XX
KM Drosophila; developmental biology; cell signalling; insecticide;
KM pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB61954.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 12653; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1301 BP; 336 A; 323 C; 366 G; 276 T; 0 U; 0 Other;

Query Match 4.7%; Score 49; DB 4; Length 1301;
Best Local Similarity 48.7%; Pred. No. 0.2;
Matches 133; Conservative 0; Mismatches 140; Indels 0; Gaps 0;
QY 494 TTGCGGGAAGAAGTTCAAAAGTTAAATTAGGAAATACAGGAATTATCGGCTTG 553
DB 742 TCGCCGGCAGTGCTGGCAAGCAGATTAATGCCATATCGATTCAACACCATATACGCTCTGG 801
QY 554 ATCTGTGAGACCGTATTTTCATCGAGTGA CTGTCCGGACAGACTTTGCCTAACAGACG 613
DB 802 ATCCGGCGGTCACAGTTCGGGAGAAAGACGACGAGTACCGAATCGATGCTAGTGACG 861
QY 614 CAGATATGTTCAAGTATATACATCAATCATATATAGAGTATATTATAATGTTGTA 673
DB 862 CCTCTATGTGAGTCCATTCAACCAAGCGTTAGCTTTGGCTTCGAGCAGCCCGTGGGAC 921
QY 674 GCGTGAATTTCTACGTGAATTATGAAAAATCAACCTGCTTGCAATGAAACATCCTGCT 733
DB 922 ACGCCACCTTCTATCCCACTATGGAAGAATCAGAGAATGCTATGTCTATGGCTGTT 981
QY 734 CTCATACGAAAGCCGTGAATATCTGACTGAGT 766
DB 982 CTCATAGAGATCCCATGACTACTTCAATAGAGT 1014

RESULT 6
ABL06056/c
ID ABL06056 standard; cDNA; 4016 BP.
XX
AC ABL06056;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 12650.
XX
KM Drosophila; developmental biology; cell signalling; insecticide;
KM pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB61953.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 12650; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 4016 BP; 1092 A; 909 C; 867 G; 1148 T; 0 U; 0 Other;

Query Match 4.7%; Score 49; DB 4; Length 4016;
Best Local Similarity 48.7%; Pred. No. 0.26;
Matches 133; Conservative 0; Mismatches 140; Indels 0; Gaps 0;
QY 494 TTGCGGGAAGAAGTTCAAAAGTTAAATTAGGAAATACAGGAATTATCGGCTTG 553
DB 1560 TCGCCGGCAGTGCTGGCAAGCAGATTAATGCCATATCGATTCAACACCATATACGCTCTGG 1501
QY 554 ATCTGTGAGACCGTATTTTCATCGAGTGA CTGTCCGGACAGACTTTGCCTAACAGACG 613
DB 1500 ATCCGGCGGTCACAGTTCGGGAGAAAGACGACGAGTACCGAATCGAATGCTAGTGACG 1441
QY 614 CAGATATGTTCAAGTATATACATCAATCATATATAGAGTATATTATAATGTTGTA 673
DB 1440 CCTCTATGTGAGTCCATTCAACCAAGCGTTAGCTTTGGCTTCGAGCAGCCCGTGGGAC 1381
QY 674 GCGTGAATTTCTACGTGAATTATGAAAAATCAACCTGCTTGCAATGAAACATCCTGCT 733
DB 1380 ACGCCACCTTCTATCCCACTATGGAAGAATCAGAGAATGCTATGTCTATGGCTGTT 1321
QY 734 CTCATACGAAAGCCGTGAATATCTGACTGAGT 766

Db	1320	CTCATAGAGATCCCATGACTACTTCATAGAGT	1288
RESULT 7			
AAH24065/c			
ID	AAH24065	standard; DNA; 4590 BP.	
XX			
AC	AAH24065;		
XX			
DT	29-AUG-2001	(first entry)	
XX			
DE	Yeast AOD9604-associated DNA sequence, SEQ ID NO:1.		
XX			
KW	Human growth hormone analogue peptide; hGH; AOD9604; lipid metabolism; modulation; lipolysis stimulation; hormone-sensitive lipase stimulation;		
KW	lipogenesis inhibition; acetyl CoA carboxylase inhibition; obesity;		
KW	functional food; transgenic yeast; fat/lean ratio; food use; ds.		
XX			
OS	Saccharomyces cerevisiae.		
XX			
FH	Key	Location/Qualifiers	
FT	misc_feature	10	
FT		/*tag= a	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	3617	
FT		/*tag= b	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	3649	
FT		/*tag= c	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	3679	
FT		/*tag= d	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	3819	
FT		/*tag= e	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	3862	
FT		/*tag= f	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	3864	
FT		/*tag= g	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	3888	
FT		/*tag= h	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	3890	
FT		/*tag= i	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	3912	
FT		/*tag= j	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	3914	
FT		/*tag= k	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	3938	
FT		/*tag= l	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	3939	
FT		/*tag= m	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	3941	
FT		/*tag= o	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	3943	
FT		/*tag= p	
FT		/note= "Represented as * in the specification"	
FT	misc_feature	4361	
FT		/*tag= q	
FT		/note= "Represented as * in the specification"	
XX			
PN	WO200133977-A1.		
XX			
PD	17-MAY-2001.		

XX 06-NOV-2000; 2000WO-AU001362.
PF
XX
PR 05-NOV-1999; 99AU-00003875.
XX
XX
PA (META-) METABOLIC PHARM LTD.
XX
PI Belyea CI, Ng FM, Vaughan P;
XX
DR WPI; 2001-328876/34.
XX
PT New organisms containing nucleic acid encoding a growth hormone fragment
PT which modulates lipid metabolism are useful to produce dietary aids for
PT obesity and in the meat production industry.
XX
PS Disclosure; Page 48-50; 54pp; English.

CC The invention relates to novel transgenic organisms useful in the
CC production of functional food and drink products for the treatment or
CC prevention of obesity via the regulation of lipid metabolism. The
CC organisms comprise a polynucleotide encoding a growth hormone fragment
CC capable of stimulating the activity of hormone-sensitive lipase (the key
CC enzyme in lipolysis) and inhibiting acetyl CoA carboxylase (the key
CC enzyme in lipogenesis). The growth hormone fragment preferably contains
CC at least the disulphide-bonded loop of a mammalian growth hormone (but is
CC not the full-length growth hormone) and is optionally linked to an
CC epitope tag or heterologous fusion protein partner. The transgenic
CC organism may be a microorganism used to produce a fermented product
CC (e.g., yeast), or an edible plant or animal or cell thereof. Food or
CC drink made using methods of the invention are used to modify fat/lean
CC ratio, lipid metabolism or food use in a mammal. In particular, the food
CC or drink products may be used to treat or prevent obesity, particularly
CC in humans, and may also be used to improve the fat/lean ration of
CC livestock raised for meat production. In the exemplification of the
CC invention, the human growth hormone (hGH) fragment analogue AOD9604 was
CC expressed in yeast, optionally fused to the FLAG epitope (AAB73625). The
CC present sequence is described as a DNA sequence from yeast in the
CC sequence listing, but is not further referred to in the specification
XX
SQ Sequence 4590 BP; 661 A; 384 C; 127 G; 522 T; 0 U; 2896 Other;

Query Match 4.5%; Score 47.4; DB 5; Length 4590;
Best Local Similarity 11.2%; Pred. No. 0.64;
Matches 82; Conservative 319; Mismatches 329; Indels 0; Gaps 0;
QY 92 TAGTATTCATGTTTACTCAAGGAGTAACGAGATGTAATATCTTAAAGAAACTT 151
Db 4466 HWRYYCTNTKGNATYASNKNATKYNRYTKKSASCHTSTNTKANHGKANHGYSANKGANKG 4407
QY 152 TAACGAATTACGATCTGTTTACAAGCTCAATATCAAAACAAGTTGTAATCTTATAC 211
Db 4406 HHYWASHHYWHAASNKHTAKHTSNATGTYTAVVSYYTDSYRVANAHHVNTCHAADGM 4347
QY 212 ATGTTTCCTTCACTGGGATATGAAGAACTTCGTTGCTATGCGAAAGCTTAAATAG 271
Db 4346 GTDDAYCHSYHYWASYGKHSRHNWGSNNHNSRHNWSSDSDSRHNWSRHNWHAHGSSATKAS 4287
QY 272 AAAAAGATGATTTCTTGAATTTCCGCTCACTGGAAGAAGGCTTGTATGCTTTTG 331
Db 4286 GHYHWASSVKDHSVVDWNYGYTYKRSNTKYWNSKACKSSWMSMWSMYHSTBTISR 4227
QY 332 CTTCACAAAGATGCTTGGGTTATTCGAAGCCGTTGGAACAACACGTCACGTTGGA 391
Db 4226 YBGYATKAGSRHNWHSBTBSRYBGYATKAGSRHNWHSBTBSRYBGYATKAGSRHNWHSB 4167
QY 392 AATTGTAGCTGAATTTTACAAACTACTGTAGAAAAATATAAGTCTGATATCAATA 451
Db 4166 TSRYBGYATKAGSRHNWHSBTBSRYBGYATKAGSRHNWHSBTBSRYBGYATKAGSRHNW 4107
QY 452 TACGATGATCGGCATAGTTTGGCGGCATACCTCAGGTTTTCGGGAAAGAAAGATTTC 511
Db 4106 HMSRHNWKSYSKRHNWMMYHVVCARRYWBHVHNMRRMWMKKKGKKGYSYVKNNTYVKNCT 4047

[illegible]

RESULT 8	
ID	ADP28939 standard; DNA; 1584 BP.
XX	ADP28939;
XX	
DT	12-AUG-2004 (first entry)
XX	
DE	Human secreted protein encoding sequence SEQ ID #937.
XX	
KW	Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW	cancer; inflammatory; immune; ds; human secreted protein.
XX	
OS	Homo sapiens.
XX	
PN	WO2004035732-A2.
XX	
PD	29-APR-2004.
PF	28-AUG-2003; 2003WO-US026780.
XX	
PR	29-AUG-2002; 2002US-0406576P.
PR	29-AUG-2002; 2002US-0406579P.
PR	29-AUG-2002; 2002US-0406585P.
PR	29-AUG-2002; 2002US-0406588P.
PR	29-AUG-2002; 2002US-0406608P.
PR	29-AUG-2002; 2002US-0406611P.
PR	29-AUG-2002; 2002US-0406612P.
PR	29-AUG-2002; 2002US-0406616P.
PR	29-AUG-2002; 2002US-0406640P.
PR	29-AUG-2002; 2002US-0406642P.
PR	29-AUG-2002; 2002US-0406646P.
PR	29-AUG-2002; 2002US-0406653P.
PR	29-AUG-2002; 2002US-0406655P.
PR	29-AUG-2002; 2002US-0406666P.
PR	17-SEP-2002; 2002US-0410946P.
PR	17-SEP-2002; 2002US-0410947P.
PR	17-SEP-2002; 2002US-0410948P.
PR	17-SEP-2002; 2002US-0410949P.
PR	17-SEP-2002; 2002US-0410953P.
PR	17-SEP-2002; 2002US-0410957P.
PR	17-SEP-2002; 2002US-0410958P.
PR	17-SEP-2002; 2002US-0410959P.
PR	17-SEP-2002; 2002US-0410960P.
PR	17-SEP-2002; 2002US-0410961P.
PR	17-SEP-2002; 2002US-0410962P.
PR	17-SEP-2002; 2002US-0411019P.
PR	17-SEP-2002; 2002US-0411022P.

PR	17-SEP-2002;	2002US-0411023P.
PR	17-SEP-2002;	2002US-0411024P.
PR	17-SEP-2002;	2002US-0411032P.
PR	17-SEP-2002;	2002US-0411035P.
PR	17-SEP-2002;	2002US-0411037P.
PR	17-SEP-2002;	2002US-0411041P.
PR	17-SEP-2002;	2002US-0411045P.
PR	17-SEP-2002;	2002US-0411046P.
PR	17-SEP-2002;	2002US-0411048P.
PR	17-SEP-2002;	2002US-0411052P.
PR	17-SEP-2002;	2002US-0411055P.
PR	17-SEP-2002;	2002US-0411073P.
PR	17-SEP-2002;	2002US-0411082P.
PR	17-SEP-2002;	2002US-0411101P.
PR	17-SEP-2002;	2002US-0411111P.
PR	18-APR-2003;	2003US-0463700P.
PR	18-APR-2003;	2003US-0463708P.
PR	18-APR-2003;	2003US-0463716P.
PR	18-APR-2003;	2003US-0463732P.
PR	02-MAY-2003;	2003US-0467199P.
PR	02-MAY-2003;	2003US-0467201P.
PR	02-MAY-2003;	2003US-0467203P.
PR	19-MAY-2003;	2003US-0471306P.
PR	19-MAY-2003;	2003US-0471336P.
PR	22-MAY-2003;	2003US-0472420P.
PR	09-JUN-2003;	2003US-0476609P.
PR	09-JUN-2003;	2003US-0476641P.
PR	08-JUL-2003;	2003US-0485218P.
PR	08-JUL-2003;	2003US-0485223P.
PR	08-JUL-2003;	2003US-0485224P.
PR	08-JUL-2003;	2003US-0485325P.
PR	14-JUL-2003;	2003US-0486446P.
PR	14-JUL-2003;	2003US-0486480P.
PR	15-JUL-2003;	2003US-0486891P.
PR	15-JUL-2003;	2003US-0486960P.
PR	08-AUG-2003;	2003US-0493341P.
PR	08-AUG-2003;	2003US-0493370P.
PR	08-AUG-2003;	2003US-0493573P.
PR	08-AUG-2003;	2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.
 Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
 Halenbeck RF, Huang MM, Kochakota S, Haislan L, Linnemann T;
 Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
 WPI; 2004-348438/32.
 New nucleic acid molecule for diagnosing, preventing or treating diseases
 such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
 genetic, bacterial and viral diseases.
 Claim 1; SEQ ID NO 937; 428bp; English.
 The present invention relates to an isolated nucleic acid molecule
 encoding a polypeptide which is believed to be cytostatic,
 antiinflammatory, immunosuppressive, antibacterial and virucidal. The
 composition and methods are useful for diagnosing, preventing and
 treating diseases such as proliferative (e.g. cancer), inflammatory,
 immune, metabolic, genetic, bacterial and viral diseases. The present
 sequence represents a human secreted protein encoding sequence. The
 present sequence is available on WIPWEB and is not in the specification.
 Sequence 1584 BP; 450 A; 363 C; 388 G; 383 T; 0 U; 0 Other;

Query Match	4.5%	Score 47.2	DB 12	Length 1584
Best Local Similarity	45.9%	Pred. No. 0.55		
Matches 212	Conservative	0	Mismatches 238	Indels 12
			Gaps	1
QY	365	CCGTTGGAACACACGTCACGTTGGAATTTGTAGCTGATTTTACAACAACTACTTGTAG	424	

Db 371 CCGCGGGCTACACCAAACTGGTGGACAGATGTGCCCGGTTTATCACTGGATGAGG 430
QY 425 AAAAATATAAGTGTGATATCAATATACGATTGATCGGCATAGTTGGCGGCATATA 484
Db 431 AGAGTTTAATACTACCTCTGGAACAATGTCCATCTCTGGATACAGCCTTGAGCCCATG 490
QY 485 CTTGAGTTTTCGGGAAAAGAAGTTCAAAAGTTAAATTTAGAAAATACAGAATAATTA 544
Db 491 CTGCTGGCATGTGACGAGAGTCTGACCAATAAG-----AAAGTCAACAGAATTA 538
QY 545 TCGGGCTTGATCCTGCTGACCGGTATTTTCATCGGAGTGAAGTGTCCGGACAGACTTTGCG 604
Db 539 CTGGCCTCGATCCAGCTGACCTAATCTTGAGTATGAGAAGCCCGAGTCTTCTC 598
QY 605 TAACAGACGCAAGATATGTTCAAGTTATACATCAATCATATATTAGAGTATATTATA 664
Db 599 CTGATGATGACGATTTGTAGACGTCTTACACACATTCACCAAGAGGTCCTTGTCGAA 658
QY 665 ATGTTGTTAGCGTTGATTTCTACGTGAATTATGGAATAAATCAACCTGGTTGCAATGAAC 724
Db 659 GCATTGGAATCCAGAAACAGTTGGGCAATGTCATTACCCGAATGAGGTACTTTTC 718
QY 725 CATCCTGCTCTCATACGAAAGCCGTGAATATCTGACTGAGTGCATATAACATGAATGTT 784
Db 719 AGCCAGATGTAAACATGAGAAAGTATCCGCGTGAATTGCAGAGAGAGACTTGGAGACA 778
QY 785 GTTTAATTGGAACACCATGGAAGAATATTTGAGCACTCCAA 826
Db 779 TGCCAATGAACACTCTTTGTGATTTCTGCCGAGATACAA 820

RESULT 9
ADQ38815
ID ADQ38815 standard; DNA; 3564 BP.

XX AC ADQ38815;
XX DT 18-NOV-2004 (first entry)
XX DE Human SNP containing myocardial infarction-associated gene, SEQ ID 478.
XX KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX KW cardiant; gene therapy; human; gene; ds.
XX OS Homo sapiens.
XX PN WO2004058052-A2.
XX PD 15-JUL-2004.
XX PF 22-DEC-2003; 2003WO-US040978.
XX PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX PA (APPL-) APPLERA CORP.
XX PI Cargill M, Devlin JJ, Iakubova O;
XX DR WPI; 2004-533949/51.
DR P-PSDB; ADQ39643.
XX PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX OS
XX PS Claim 7; SEQ ID NO 478; 145bp; English.
XX CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of

CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX SQ Sequence 3564 BP; 1021 A; 737 C; 802 G; 985 T; 0 U; 19 Other;

Query Match 4.5%; Score 47; DB 13; Length 3564;
Best Local Similarity 50.7%; Pred. No. 0.74;
Matches 144; Conservative 1; Mismatches 127; Indels 12; Gaps 1;

QY 365 CCGTGGAAACACACGTCACGTTGGAATAATTGTAGCTGATTTTCAAAAACACTACTGTTAG 424
Db 559 CCGCGGCTACACCAAACTGTGGACAGAGATGTNGCCCGTTTATCAACTGATGAGG 618
QY 425 AAAAATATAAGTGTGATATCAATATACGATTGATCGGCAATAGTTGGCGGCATATA 484
Db 619 AGGARTTTAATCACTCCCTCTGACAATGTCCATCTCTGGGATACAGCCTTGAGCCCATG 678
QY 485 CTTGAGTTTTCGGGAAAAGAAGTTCAAAAGTTAAATTTAGAAAATACAGAATAATTA 544
Db 679 CTGCTGGCATGTGACGGAAGTCTGACCAATAAG-----AAAGTCAACAGAATTA 726
QY 545 TCGGCTTGATCCTGCTGACCGGTATTTTCATCGGAGTGAAGTGTCCGGACAGACTTTGCG 604
Db 727 CTGGCCTCGATCCAGCTGACCTAATCTTGAGTATGAGAAGCCCGAGTGTCTTCTC 786
QY 605 TAACAGACGCAAGATATGTTCAAGTTATACATCAATCAATCATATA 648
Db 787 CTGATGATGACGATTTTGTAGACGTCTTACACACATTCACCGAGA 830

RESULT 10
ABL60540
ID ABL60540 standard; cDNA; 1526 BP.

XX AC ABL60540;
XX DT 27-AUG-2002 (first entry)
XX DE Human lipid metabolism enzyme (LME)-4 cDNA (clone id: 7482937CB1).
XX KM Human; lipid metabolism enzyme; LME; cytosolic; neuroprotective; gene;
KW nootropic; cerebroprotective; antiparkinsonian; antialzheimer's; vaccine;
KW antisclerotic; antimicrobial; anti-AIDS; cardiovascular; antianginal;
KW gene therapy; protein therapy; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 259..1365
FT /*tag= a
FT /product= "lipid metabolism enzyme"

/note= "LME-4"

FT XX WO200229036-A2.
PN XX 11-APR-2002.
PD XX
PF 05-OCT-2001; 2001WO-US031302.
XX
XX 06-OCT-2000; 2000US-0238388P.
PR 13-OCT-2000; 2000US-0240616P.
PR 02-NOV-2000; 2000US-0245719P.
PR 08-NOV-2000; 2000US-0247503P.
PR 17-NOV-2000; 2000US-0249503P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Harland J, Arvizu C, Das D, Griffin JA, Baughn MR, Ding L;
PI Walia NK, Yao MG, Lu Y, Elliott VS, Thangavelu K, Ramkumar J;
PI Lal PG, Tribouley CM;
XX
XX WPI; 2002-315862/35.
DR P-PSDB; ABB08004.
XX
XX
PT Lipid Metabolism Enzymes and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, Alzheimer's disease and Creutzfeld-
PT Jakob disease.
XX
XX
PS Claim 5; Page 123; 127pp; English.
XX
XX The invention relates to human lipid metabolism enzymes (LMEs) and
CC encoding polynucleotides. The LMEs can be expressed by standard
CC recombinant technology. The LME polypeptides, polynucleotides and
CC modulators may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate LME expression such as cancer
CC (e.g. myeloma, sarcoma and breast cancer), neurological disorders (e.g.
CC Parkinson's, Alzheimer's and multiple sclerosis), microbial infections
CC (e.g. Creutzfeld-Jakob disease and Acquired Immune deficiency syndrome
CC (AIDS)) and/or cardiovascular disorders (e.g. cardiomyopathy, angina
CC pectoris and mitral valve prolapse). The present sequence represents the
CC human LME-4 encoding cDNA
XX
SQ Sequence 1526 BP; 440 A; 303 C; 325 G; 458 T; 0 U; 0 Other;

Query Match 4.5%; Score 46.8; DB 6; Length 1526;
Best Local Similarity 49.7%; Pred. No. 0.68;
Matches 160; Conservative 0; Mismatches 147; Indels 15; Gaps 1;

QY 318 TTGTAATGCTTTTGTCTCAACAAGATGCTTGGGTTATCCAAAGCCGTTGAAACAC 377
DB 312 TTGCATTAATTAGATTGATCAACGGTTCACGGGATACATCATGCTGTAAACAATCT 371
QY 378 ACGTCAAGTTGAAAATTGTAGCTGATTTTACAAAACCTAGTTAGAAAAATATAAGT 437
DB 372 CCGTGTGTTGGTGCTGAGGTGCTTATTTATTGATGTTCTCATGAAAAAATTGAATA 431
QY 438 GCTGATATCAAAATATACGATTGATCGGCATAGTTGGCGGCATACCTTCAAGTTTGC 497
DB 432 TTCCCTTCTAAAGTGACATTGATGGCCACAGCTTGGAGACACACCTGGCGGGAAGC 491
QY 498 GGGAAAGAAGTTCAAAAGTTAAATTAGAAAAATACAGAAATTATCGGCTTGATCC 557
DB 492 TGG-----GTCAAGATACCAAGCCCTTGAGAATAAATACTGGTTGAACCC 536
QY 558 TGCTGACCGTATTTTCATCGAGTGAAGTCCGACAGACTTTGCGTAACAGACGAGA 617
DB 537 AGCTGGGCCATTTTCCACAACACTCCAAAGAGTCAAGCTAGACCCCTCGATGCCAA 596
QY 618 ATATGTTCAAGTTATACATACA 639
DB 597 CTTGTGACGTTATTCATACA 618

RESULT 11

ACH03823
ID ACH03823 standard; cDNA; 3635 BP.
XX
XX AC ACH03823;
XX
XX 26-SEP-2003 (first entry)
DT
XX
DE Human cDNA differentially expressed in lung cancer #28.
XX
XX Gene therapy; emphysema; ss; gene; chronic obstructive pulmonary disease;
KM respiratory disorder; lung cancer; asthma; human.
XX
XX Homo sapiens.
OS
XX US2003065157-A1.
PN
XX
XX 03-APR-2003.
PD
XX
XX 04-APR-2002; 2002US-00116802.
PF
XX
XX 04-APR-2001; 2001US-0281593P.
PR
XX
XX (LASE/) LASEK A W.
PA
XX
XX Lasek AW;
PI
XX
XX WPI; 2003-540803/51.
DR
XX
XX
PT New combination comprising cDNAs that are differentially expressed in
PT respiratory disorders, useful for diagnosing or treating respiratory
PT disorders e.g., lung cancer, chronic obstructive pulmonary disease,
PT emphysema or asthma.
XX
XX
PS Claim 1; Page; 39pp; English.
XX
XX The invention relates to a combination comprising cDNAs or their
CC complements that are differentially expressed in respiratory disorder.
CC The combination is useful for preparing a composition for diagnosing or
CC treating respiratory disorders e.g. lung cancer, chronic obstructive
CC pulmonary disease, emphysema or asthma. The present sequence represents
CC human cDNA differentially expressed during lung cancer
XX
SQ Sequence 3635 BP; 1053 A; 752 C; 824 G; 1006 T; 0 U; 0 Other;

Query Match 4.5%; Score 46.8; DB 9; Length 3635;
Best Local Similarity 51.1%; Pred. No. 0.83;
Matches 145; Conservative 0; Mismatches 127; Indels 12; Gaps 1;

QY 365 CCGTGAACAACACACGTCAGCTTGAATAATTGTAGCTGATTTTACAACAACTAGTAG 424
DB 620 CCGCGGGCTACACCAAACTGGTGGAGACAGATGTGCCCGTTTATCACTGATGAGG 679
QY 425 AAAAATATAAAGTCTGATATCAATATACGATTGATCGGGCATAGTTGGCGCCGATA 484
DB 680 AGGAATTTAACTACCTCTGGAACAATGTCCATCTTTGGGATACAGCCTTGAAGCCCATG 739
QY 485 CTTCAAGTTTGGCGGAAAAGAGTTCAAAAGTTAAATTAGAAAATACAGGAATTA 544
DB 740 CTGCTGGCATTGACAGGAAGTCTGACCAATAG-----AAAGTCAACAGAAATTA 787
QY 545 TCGGCGCTGATCTCGCTGACCGGTATTTTCATCGGAGTGAAGTGTCCGACAGACTTGGC 604
DB 788 CTGGCCTGATCCAGCTGACCTTAACCTTGAATGACAGAAAGCCCGAGTGTCTTCTC 847
QY 605 TAAACAGACGAGATATGTTCAAGTTATACATCAATCATATA 648
DB 848 CTGATGATGACAGATTTTGAAGCGTCTTACACACATTCACCAGA 891

RESULT 12
ABL33713
ID ABL33713 standard; DNA; 13326 BP.
XX

Db 896 RRRRWTVKMSWRMYTMTKMAWTMTTCMAKMYMATGNA TWMMWRYTMYTCYAMTCA 837
Qy 373 AACACACGTCACGTTGGAAAAATTGAGCTGATTTTACAAAATACTTGTAGAAAAATAT 432
Db 836 KCKYKAMATKMTTACAMRATSWRFRAMAGMRWKRYKMKRAYWWRWRCWKAGMARWMK 777
Qy 433 ---AAAGTCTGATATCAAAATATAGATTGATCGGGCATAGTTGGCGGCATCTTC 488
Db 776 SRYRWKMKYATRYWKMAMTWMSWRWKS YRMWSGMRWSAMRYCSRMCAKTKY 717
Qy 489 AGTTTTCGGGAAAAAGATTCAAAAGTTAAAAATTAGAAAAATACAAGAAATTATCGG 548
Db 716 ASSARWTK-RAKRSYRARRRWYKRGWTTYRYRWRSCTMRARMSKRKRWAGASMKSCW 658
Qy 549 GCTTGATCCTGCTGACCGTATTTTCATCGGAGTGACTGTCCGACAGACTTGGCTAAC 608
Db 657 MYWRGARSMMYSKYSASAACCKTRRYMTSSYMTSGMYGMYSSYKSMSTSKMSTMGKMT 598
Qy 609 AGACGCAATATGTTCAAGTTATACATACATCAATCATATTAGAGTATATTAATGT 668
Db 597 TMYTSMKSTRRSKMGWMSGMSMYMRWMMKMRKRKYMRMYKWKCTWRRCMYRWGYTMY 538
Qy 669 TGGTAGCCTGATTTCTACGTGAATTAATGAAAAAATCAACCTGTTGCAATGAACCATC 728
Db 537 TTSRSRWMTGRYKARYTSKRRYWYKYRKYCWMYYYGMYMKCSYMRGYCKACKCCY 478
Qy 729 CTGCTCTCATACGAAACCGTGAATAATCTGACTGAGTCATAAACATGAATGTTGTTT 788
Db 477 AMCWKAAYSGMMYMYRYKYSKMWMSTKYMMSMWYKKCRSMKYGAKGCGYCKMWTYCSYG 418
Qy 789 AATTGGAACACCATGGAAGAATATTTCAGCACTCCAAAACCAATTTCCAGTGAAGAGG 848
Db 417 YMKWYTYMGSYKYSRCKYKMYMYKGMWYMYMYSAYSMMTWYYYAKYWKYKRGRT 358
Qy 849 AGACACCTGTGTTTGCGTTGGATTGAATGCAAAAAGTTATCTGCTAGAGCGCATTTTA 908
Db 357 MSWYGSYKKKYCTWCMYMKCMRCYRWKMRKTKYSKRCYCWRYATCYWCCCYRKRGM 298
Qy 909 TGCACCGGTTGAAGCAAAATGCACCTTAAT 937
Db 297 YSRSMMRTAGKWKMRWSRWCSYSWYK 269

RESULT 14
ABA92788
ID ABA92788 standard; DNA; 7786 BP.
XX ABA92788;
AC
XX
DT 27-MAR-2002 (first entry)
XX
DE Buchnera sp. plasmid pIeu DNA sequence SEQ ID NO:2.
XX
KW Buchnera; cockroach-symbiotic bacterium; cockroach extermination;
XX circular; ds.
OS Buchnera sp.
XX
FH Key location/Qualifiers
FT CDS complement(346..1197)
FT CDS /*tag= a
FT CDS /product= "repa1 protein"
FT CDS 1514..2017
FT CDS /*tag= b
FT CDS /product= "yqha protein"
FT CDS 2357..2893
FT CDS /*tag= c
FT CDS /product= "repa2 protein"
FT CDS 3032..4591
FT CDS /*tag= d
FT CDS /product= "leua protein"
FT CDS 4652..5743
FT CDS /*tag= e

FT /product= "leub protein"
FT CDS 5733..7160
FT /*tag= f
FT /product= "leuc protein"
FT CDS 7163..7786
FT /*tag= g
FT /product= "leud protein"
PN JP2001292771-A.
XX
PD 23-OCT-2001.
XX
PF 07-APR-2000; 2000JP-00107160.
XX
PR 07-APR-2000; 2000JP-00107160.
XX
PA (RIKA) RIKAGAKU KENKYUSHO.
XX
DR WPI; 2002-126043/17.
XX
PT A genomic DNA of cockroach-symbiotic bacterium.
XX
PS Claim 5; Page 230-233; 237pp; Japanese.
XX
CC The present invention describes a gene (I) derived from Buchnera sp.
CC containing the DNA (a) or (b), (a) has a fully defined base pair sequence
CC selected from a table of sequences found in the Buchnera sp. genomic DNA
CC of ABA92787 given in the specification or is a DNA selected from
CC complementary DNA sequences, and (b) is a DNA which hybridises with the
CC DNA (a) and encodes a protein. Also described are: (1) a recombinant
CC vector (II) containing (I); (2) a transformant (III) containing (II); (3)
CC a genomic DNA of Buchnera sp. containing the sequence given in ABA92787;
CC (4) a plasmid derived from Buchnera sp. containing DNA (c) or (d), (c) is
CC a DNA containing a fully defined sequence given in ABA92788 or ABB92789
CC and (d) is a plasmid which hybridises with a DNA; and (5) a method for
CC the preparation of a protein in which (III) is cultured and the
CC expression protein of the objective protein is collected from the
CC resultant culture. The DNA is useful for developing agricultural
CC chemicals for exterminating cockroaches. The present sequence represents
CC the specifically claimed Buchnera sp. plasmid pIeu, from the present
XX invention
SQ Sequence 7786 BP; 2887 A; 867 C; 1213 G; 2819 T; 0 U; 0 Other;

Query Match 4.4%; Score 45.8; DB 6; Length 7786;
Best Local Similarity 51.4%; Pred. No. 1.7;
Matches 133; Conservative 0; Mismatches 122; Indels 4; Gaps 1;
Qy 70 TGTACTTTTAATGAGAAAGATATAGTATTTCTATGTTTACTCAAGGATAGCGAGATGCT 129
Db 1229 TTTTATATATTTTCAAAATATATAAAATTTTATTTTATTTCTTCAATATATAAATTTT 1288
Qy 130 ATTATTTCTTAAGAAAGAACTTTAAGCAATTAGCATCTGTTACAAAGTCTACAATATCA 189
Db 1289 TTATATTTTAAGATATATATCTTACTTTATTTTATTTTATGAATAAATATATTTATTA 1348
Qy 190 AAACAAGTTGTATTTCTTATACA---TGGTTTCCTTCAACTGGGAATTAAGAAAACCTT 245
Db 1349 AAAATTAATATATTTTACATACATTTTGATTAATTTTCAACGATTAACATAAACTT 1408
Qy 246 CGTTGCTATGTCGAAAGCTTTAATAGAAAAAGATGATTTTCTGTAAATTTGGTGAAGT 305
Db 1409 AAAAGTTTATCTTAACCTTCTTAATTAATAATAATATATTTATTAATCAATCTATAT 1468
Qy 306 GAAGAAGGTGCTGTGAAT 324
Db 1469 CAAAAACAATATTTTAT 1487

RESULT 15
AD123669
ID AD123669 standard; cDNA; 1383 BP.

AC ADI23669;
XX
DT 06-MAY-2004 (first entry)
XX
DE Mouse LPDL CDNA #2.
XX
KW lipase; LPDL; LPDLR; lipase deficiency; atherosclerosis;
KW fatty liver disease; dyslipidaemia; hypercholesterolaemia;
KW hypertriglyceridaemia; mixed dyslipidaemia; lipid deficient state;
KW lipoprotein deficient state; mouse; gene; ss.
XX
OS Mus sp.
XX
PN WO2003055995-A2.
XX
PD 10-JUL-2003.
XX
PF 23-DEC-2002; 2002WO-CA001998.
XX
PR 21-DEC-2001; 2001US-0341786P.
PR 10-JAN-2002; 2002US-0346603P.
XX
PA (WENX/) WEN X.
PA (STEW/) STEWART A K.
PA (TSUI/) TSUI L.
PA (HEGE/) HEGELE R A.
XX
PI Wen X, Stewart AK, Tsui L, Hegele RA;
XX
DR WPI: 2003-569444/53.
DR P-PSDB; ADI23670.
XX
PT Novel isolated LPDL or LPDLR lipase polypeptides, useful for identifying
PT substances that bind to the protein and which are useful for treating
PT diseases associated with lipase function e.g. atherosclerosis and
PT hypercholesterolemia.
XX
PS Claim 3; SEQ ID NO 5; 172pp; English.
XX
CC The invention relates to an isolated mammalian (e.g., human or mouse)
CC lipase polypeptide (polyp), e.g., LPDL (I) or LPDLR polyp (II). (I) or
CC (II) is useful for identifying substances which can bind with LPDL or
CC LPDLR polyp, and for identifying a compound that affects the binding of
CC LPDL or LPDLR polyp and an LPDL or LPDLR binding polyp. (I) or (II) or
CC their nucleic acid is useful for identifying a compound that affects LPDL
CC or LPDLR polyp activity or expression. (I) or (II) or their nucleic acid
CC is useful for detecting or monitoring a condition associated with
CC increased or decreased LPDL or LPDLR expression or activity in an animal,
CC where the condition is lipase deficiency, atherosclerosis, fatty liver
CC disease and dyslipidemias, such as hypercholesterolemia,
CC hypertriglyceridaemia, mixed (combined) dyslipidaemia, lipid or lipoprotein
CC deficient states, and/or any other tissue or plasma disorders of lipid or
CC lipoprotein metabolism. The nucleic acid is useful for diagnosing the
CC presence of or a predisposition for a disorder in a subject which
CC involves detecting a germline alteration in the nucleic acid in the
CC subject. An inhibitor is useful for modulating triglyceride activity by
CC inhibiting expression or activity of (I) or (II). The nucleic acid is
CC useful as a probe or primer. The present sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 1383 BP; 423 A; 273 C; 277 G; 410 T; 0 U; 0 Other;

Query Match	4.4%;	Score 45.6;	DB 10;	Length 1383;
Best Local Similarity	51.9%;	Pred. No. 1.3;		
Matches 161; Conservative	0;	Mismatches 134;	Indels 15;	Gaps 2;

OY	448	AATATACGATTGATCGGGCATAGTTTGGCGGCATACTTCAGSTTTTGCGGAAAGA	507
Db	466	AATTTCACTTCATTGGCATTGAGCTTAGGGGCTCATATTAGTGAATTGTAGAAAGATA	525
OY	508	GTTCAAAGTTAAATTAGAAAATACAAGAAATTATCGGCTTGATCCTGCTGACC	567
Db	526	TTTCA-----TGTCACCTTGGAAGAAATTACAGGCTTGACCCAGCTGACCA	573

QY 568 TATTTTCATCGGAGTGACTGTGCCGACAGACTTTGCCGTAACAGACGCAGAAATATGTTCAA 627

Db 574 CAATTTTCTAGAAAGCCATCGAATAGCAGATTATATTACACAGATGCAAAGTTTGATGAT 633

QY 628 GTTATACATACATCAATCATATA--TTAGAGTATATTATAATGTTGTAGCGTTGATTTTC 684

Db 634 GTCATCCACACTGATATATCAAAAGTTGGGTATTGGAGAGCCATCGGGCACATTGATTTT 693

QY 685 TACGTGAATTATGGA AAAAATCAACCTGGTTGCAATGAACCATCCTCTCATACGAAA 744

Db 694 TATCCAAATGAGGAA AACAATCAGCCAGGTGTCTTACATCAATTTTTCAGGAACCAAT 753

QY 745 GCCGTGAAT 754

Db 754 TTTATTAAAT 763

Search completed: April 28, 2005, 20:21:10
Job time : 684 secs

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OM nucleic - nucleic search, using sw model

Run on: April 28, 2005, 19:29:29 ; Search time 221 Seconds

(without alignments)
7759.357 Million cell updates/sec

Title: US-10-688-011-1

Perfect score: 1048

Sequence: 1 attgcttctgttagatga.....agtcataataaaaaaaaaa 1048

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	1048	3	US-09-166-205B-63
2	1048	100.0	1048	4	US-09-806-658-1
3	441	42.1	1050	1	US-08-180-209B-16
4	441	42.1	1050	1	US-08-385-745-16
5	441	42.1	1050	3	US-08-485-388-16
6	441	42.1	1050	3	US-08-474-853-16
7	441	42.1	1050	3	US-09-166-205B-16
8	441	42.1	1050	5	PCT-US94-02629-16
9	426.2	40.7	1341	1	US-08-180-209B-26
10	426.2	40.7	1341	1	US-08-385-745-26
11	426.2	40.7	1341	3	US-08-485-388-26
12	426.2	40.7	1341	3	US-08-474-853-26
13	426.2	40.7	1341	3	US-09-166-205B-26
14	426.2	40.7	1341	5	PCT-US94-02629-26
15	59	5.6	1141	4	US-09-806-708B-22
16	47.8	4.6	5096	4	US-09-949-016-15105
17	46.4	4.4	1141	4	US-09-806-708B-22
18	45.8	4.4	7786	4	US-09-790-988-2
19	45.2	4.3	1401	4	US-09-411-132A-2
20	45.2	4.3	2352	4	US-09-411-132A-1
21	45.2	4.3	3549	4	US-09-054-272-39
22	44.4	4.2	1603	4	US-09-949-016-35
23	44.2	4.2	1767	4	US-09-601-198-72
24	43.6	4.2	1493	1	US-08-340-820-24
25	43.6	4.2	1493	1	US-08-593-535-24
26	42.2	4.0	601	4	US-09-949-016-201237
27	42.2	4.0	601	4	US-09-949-016-201351

28	42.2	4.0	1168	4	US-09-270-767-662	Sequence 662, App
29	42.2	4.0	1168	4	US-09-270-767-15944	Sequence 15944, A
30	42.2	4.0	145241	4	US-09-949-016-17394	Sequence 17394, A
31	42.2	4.0	145241	4	US-09-949-016-17395	Sequence 17395, A
32	42	4.0	36159	3	US-09-749-588-3	Sequence 3, Appli
33	42	4.0	36159	4	US-10-135-687-3	Sequence 3, Appli
34	41.4	4.0	505	4	US-09-417-251A-3	Sequence 3, Appli
35	41.4	4.0	1659	4	US-09-949-016-4553	Sequence 4553, Ap
36	41	3.9	832	4	US-09-621-976-2813	Sequence 2813, Ap
37	40.8	3.9	72278	4	US-09-949-016-16113	Sequence 16113, A
38	40.6	3.9	1771	4	US-09-907-794A-158	Sequence 158, App
39	40.6	3.9	1771	4	US-09-866-028-36	Sequence 36, Appl
40	40.6	3.9	1771	4	US-09-905-125A-158	Sequence 158, App
41	40.6	3.9	1771	4	US-09-902-775A-158	Sequence 158, App
42	40.6	3.9	1771	4	US-09-906-700-158	Sequence 158, App
43	40.6	3.9	1771	4	US-09-944-457-36	Sequence 36, Appl
44	40.6	3.9	1771	4	US-09-903-603A-158	Sequence 158, App
45	40.6	3.9	1771	4	US-09-904-920A-158	Sequence 158, App

ALIGNMENTS

RESULT 1									
US-09-166-205B-63									
; Sequence 63, Application US/09166205B									
; Patent No. 6372471									
; GENERAL INFORMATION:									
; APPLICANT: Te Piao KING									
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES,									
; TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL									
; TITLE OF INVENTION: THERAPIES BASED THEREON									
; FILE REFERENCE: 2313/0F138US									
; CURRENT APPLICATION NUMBER: US/09/166, 205B									
; CURRENT FILING DATE: 1998-10-01									
; NUMBER OF SEQ ID NOS: 70									
; SOFTWARE: FastSeq for Windows Version 3.0									
; SEQ ID NO 63									
; LENGTH: 1048									
; TYPE: DNA									
; ORGANISM: Polistes annularis									
US-09-166-205B-63									
Query Match									
Best Local Similarity 100.0%; Score 1048; DB 3; Length 1048;									
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	ATTGCTTCTGTTAGATGATTCGACGACATTGAGAAATGCTGACCTTGATAGAGCATG	60						
Db	1	ATTGCTTCTGTTAGATGATTCGACGACATTGAGAAATGCTGACCTTGATAGAGCATG	60						
Qy	61	TCTCCGATTGTACTTTTAATGAGAAAGATATAGTATTCTATGTTACTCAAGGATAG	120						
Db	61	TCTCCGATTGTACTTTTAATGAGAAAGATATAGTATTCTATGTTACTCAAGGATAG	120						
Qy	121	CGAGATGTATTATTCTTAAGAAAGAACTTAAAGAAATTACGATCTGTTACAAAGTCT	180						
Db	121	CGAGATGTATTATTCTTAAGAAAGAACTTAAAGAAATTACGATCTGTTACAAAGTCT	180						
Qy	181	ACAATATCAAAACAAGTTGTTTCTTATACATGTTCTTCAACTGGAATAATGAA	240						
Db	181	ACAATATCAAAACAAGTTGTTTCTTATACATGTTCTTCAACTGGAATAATGAA	240						
Qy	241	AACCTCGTGTCTATGTCGAAAGCTTATATAGAAAGATGATTTCTTGAATTCGGTC	300						
Db	241	AACCTCGTGTCTATGTCGAAAGCTTATATAGAAAGATGATTTCTTGAATTCGGTC	300						
Qy	301	GACTGGAAGAAGGCTGCTTGAATGCTTTGCTTCAACAAAGATGCTTTGGTATTCC	360						
Db	301	GACTGGAAGAAGGCTGCTTGAATGCTTTGCTTCAACAAAGATGCTTTGGTATTCC	360						
Qy	361	AAAGCCGTGGAACACAGCTCAGTTGAAAAATTGTAGCTGATTTTCAAACTACTT	420						

Db 361 AAAGCCGTGGAAACACACGTCACGTTGMAAAATTGTAGCTGATTTTACAAAACACTACTT 420
QY 421 GTAGAAAAATATAAAGTGTGATATCAATATATCGATTGATCGGCGCATAGTTGGCGCG 480
Db 421 GTAGAAAAATATAAAGTGTGATATCAATATATCGATTGATCGGCGCATAGTTGGCGCG 480
QY 481 CATACTTCAGGTTTTCGCGGAAAAGAGTTCAAAAGTTAAATTTAGGAAAATACAGAGAA 540
Db 481 CATACTTCAGGTTTTCGCGGAAAAGAGTTCAAAAGTTAAATTTAGGAAAATACAGAGAA 540
QY 541 ATTATCGGGCTTGATCTGCTGGAACCGTATTTTCATCCGAGTGACTGTCGCGACAGACTT 600
Db 541 ATTATCGGGCTTGATCTGCTGGAACCGTATTTTCATCCGAGTGACTGTCGCGACAGACTT 600
QY 601 TCGGTAACAGACGACGAGATATGTTCAAGTTATACATCAATCATATTTAGAGATATAT 660
Db 601 TCGGTAACAGACGACGAGATATGTTCAAGTTATACATCAATCATATTTAGAGATATAT 660
QY 661 TATATGTTGGTAGCGTTGATTTCTACGTAATTATGMAAAATCAAACCTGCTGCAAT 720
Db 661 TATATGTTGGTAGCGTTGATTTCTACGTAATTATGMAAAATCAAACCTGCTGCAAT 720
QY 721 GAACCATCTGCTCTCATACGAAAGCCGTGAATAATCTGACTGAGTGCAATAAACATGAA 780
Db 721 GAACCATCTGCTCTCATACGAAAGCCGTGAATAATCTGACTGAGTGCAATAAACATGAA 780
QY 781 TGTGTTTAAATGGAACCATGGAAGAATATTTACGACTCCAAAACCAATTTCCAG 840
Db 781 TGTGTTTAAATGGAACCATGGAAGAATATTTACGACTCCAAAACCAATTTCCAG 840
QY 841 TGCAGAGAGACACCTGTGTTTTCGCTTGATGCAATGCAAAAAGTTATCTGCTAGAGGC 900
Db 841 TGCAGAGAGACACCTGTGTTTTCGCTTGATGCAATGCAAAAAGTTATCTGCTAGAGGC 900
QY 901 GCATTTTATGCAACCGGTGAAGCAATGCACTTATTTGCCATTAACGAGGGGATTAACTT 960
Db 901 GCATTTTATGCAACCGGTGAAGCAATGCACTTATTTGCCATTAACGAGGGGATTAACTT 960
QY 961 TAAATTATTAACAAAAGTCAATGTACACAAAATGTATCTATTGATGAATTAATGAAT 1020
Db 961 TAAATTATTAACAAAAGTCAATGTACACAAAATGTATCTATTGATGAATTAATGAAT 1020
QY 1021 AAACGAACAGTCAAAATTAATAAAAAA 1048
Db 1021 AAACGAACAGTCAAAATTAATAAAAAA 1048

RESULT 2
US-09-806-658-1
; Sequence 1, Application US/09806658
; Patent No. 6652851
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF POLISTINAE VENOM ENZYMES, S
; FILE REFERENCE: 2313/1F138-US1
; CURRENT APPLICATION NUMBER: US/09/806, 658
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Polistes annularis
; US-09-806-658-1

Query Match 100.0%; Score 1048; DB 4; Length 1048;
Best Local Similarity 100.0%; Pred. No. 3.9e-268;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 TCTCCGATTGTACTTTTAAATGAGAAAGATATAGTATTTCTATGTTTAACTCAAGGATAG 120
Db 61 TCTCCGATTGTACTTTTAAATGAGAAAGATATAGTATTTCTATGTTTAACTCAAGGATAG 120
QY 121 CGAGATGTAATATCTTAAGAAAGAACTTTAACGAATTACGATCTGTTTACAAAGCT 180
Db 121 CGAGATGTAATATCTTAAGAAAGAACTTTAACGAATTACGATCTGTTTACAAAGCT 180
QY 181 ACAATATCAAAACAAGTTGATTTCTTAATACATGTTTCTTCAACTGGGAATTAATGAA 240
Db 181 ACAATATCAAAACAAGTTGATTTCTTAATACATGTTTCTTCAACTGGGAATTAATGAA 240
QY 241 AACTTCGTTGCTATGTCGAAAGCTTTAATAGAAAAAGATGATTTCTGTAATTTCCGTC 300
Db 241 AACTTCGTTGCTATGTCGAAAGCTTTAATAGAAAAAGATGATTTCTGTAATTTCCGTC 300
QY 301 GACTGGAAGAGGTCCTGTAATGCTTTTCTCAACAAAGATGCTTTGGTTATTC 360
Db 301 GACTGGAAGAGGTCCTGTAATGCTTTTCTCAACAAAGATGCTTTGGTTATTC 360
QY 361 AAAGCCGTGGAAACACACGTCACGTTGGAATAATTGTAGCTGATTTTACAAAACACTATT 420
Db 361 AAAGCCGTGGAAACACACGTCACGTTGGAATAATTGTAGCTGATTTTACAAAACACTATT 420
QY 421 GTAGAAAAATATAAGTCTGATATCAATATATACGATTGATCGGCGATAGTTGGCGCG 480
Db 421 GTAGAAAAATATAAGTCTGATATCAATATATACGATTGATCGGCGATAGTTGGCGCG 480
QY 481 CATACTTCAGGTTTTCGCGGAAAAGAGTTCAAAAGTTAAATTTAGAAAAATACAAAGAA 540
Db 481 CATACTTCAGGTTTTCGCGGAAAAGAGTTCAAAAGTTAAATTTAGAAAAATACAAAGAA 540
QY 541 ATTATCGGGCTTGATCTGCTGACCGGTATTTTCATCGGAGTGACTGTCCGACAGACTT 600
Db 541 ATTATCGGGCTTGATCTGCTGACCGGTATTTTCATCGGAGTGACTGTCCGACAGACTT 600
QY 601 TGCCTAACAGACGACGAGATATGTTCAAGTTATACATACATCAATCATATTAGAGATATAT 660
Db 601 TGCCTAACAGACGACGAGATATGTTCAAGTTATACATACATCAATCATATTAGAGATATAT 660
QY 661 TATATGTTGGTAGCGTTGATTTCTACGTAATTATGMAAAATCAAACCTGCTGCAAT 720
Db 661 TATATGTTGGTAGCGTTGATTTCTACGTAATTATGMAAAATCAAACCTGCTGCAAT 720
QY 721 GAACCATCTGCTCTCATACGAAAGCCGTGAATAATCTGACTGAGTGCATAAAAACATGAA 780
Db 721 GAACCATCTGCTCTCATACGAAAGCCGTGAATAATCTGACTGAGTGCATAAAAACATGAA 780
QY 781 TGTGTTTAAATGGAACCATGGAAGAATATTTACGACTCCAAAACCAATTTCCAG 840
Db 781 TGTGTTTAAATGGAACCATGGAAGAATATTTACGACTCCAAAACCAATTTCCAG 840
QY 841 TGCAGAGAGACACCTGTGTTTTCGCTTGATGCAATGCAAAAAGTTATCTGCTAGAGGC 900
Db 841 TGCAGAGAGACACCTGTGTTTTCGCTTGATGCAATGCAAAAAGTTATCTGCTAGAGGC 900
QY 901 GCATTTTATGCAACCGGTGAAGCAATGCACTTATTTGCCATTAACGAGGGGATTAACTT 960
Db 901 GCATTTTATGCAACCGGTGAAGCAATGCACTTATTTGCCATTAACGAGGGGATTAACTT 960
QY 961 TAAATTATTAACAAAAGTCAATGTACACAAAATGTATCTATTGATGAATTAATGAAT 1020
Db 961 TAAATTATTAACAAAAGTCAATGTACACAAAATGTATCTATTGATGAATTAATGAAT 1020
QY 1021 AAACGAACAGTCAAAATTAATAAAAAA 1048
Db 1021 AAACGAACAGTCAAAATTAATAAAAAA 1048

QY 1 ATTTGCTTCTGTTAGATGATTCGACGACATTTAGAAATGTTACCTTGAATAGAGGCATG 60
Db 1 ATTTGCTTCTGTTAGATGATTCGACGACATTTAGAAATGTTACCTTGAATAGAGGCATG 60

RESULT 3
US-08-180-209B-16
; Sequence 16, Application US/08180209B


```

: Patent No. 5593877
:
: GENERAL INFORMATION:
:
: APPLICANT: King, Te-Piao
:
: TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
:
: TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
:
: TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED
:
: TITLE OF INVENTION: THEREON
:
: NUMBER OF SEQUENCES: 62
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: Klauber & Jackson
:
: STREET: 411 Hackensack Avenue
:
: CITY: Hackensack
:
: STATE: New Jersey
:
: COUNTRY: USA
:
: ZIP: 07601
:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC compatible
:
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: PatentIn Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/08/180,209B
:
: FILING DATE: 11-JAN-1994
:
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
:
: APPLICATION NUMBER: US 08/031,400
:
: FILING DATE: 11-MAR-1993
:
: ATTORNEY/AGENT INFORMATION:
:
: NAME: Jackson Esq., David A.
:
: REGISTRATION NUMBER: 26,742
:
: REFERENCE/DOCKET NUMBER: 600-1-074 CIP
:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: 201 487-5800
:
: TELEFAX: 201 343-1684
:
: TELEX: 133521
:
: INFORMATION FOR SEQ ID NO: 16:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 1050 base pairs
:
: TYPE: nucleic acid
:
: STRANDEDNESS: single
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: cDNA
:
: FEATURE:
:
: NAME/KEY: CDS
:
: LOCATION: 1..951
:
: US-08-180-209B-16

```

```

Query Match          42.1%; Score 441; DB 1; Length 1050;
Best Local Similarity 67.0%; Pred. No. 4e-107;
Matches 665; Conservative 0; Mismatches 310; Indels 18; Gaps 2;

```

```

QY      65  CCGATTGTACTTTAATGAGAAAGATATAGTATTCTATGTTTACTCAAGGGAAGCGAG 124
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      56  CCGTATGTCCCTTAGTATGATACAGTTAAGATGATTTTAAACAAGGAAACCGAA 115
QY      125 ATGGTATTATTCTTAAGAAAGAACTTTAACGAATTACGATCTGTTACAAAGTCTACAA 184
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      116 AACATGATTTTATACGCTGATACATGAACACAGGCAATGAATTTAAGAGTCAATCA 175
QY      185 TATCAAAACAAGTGTATTCTTATACATGTTTCTTCAACTGGAAATAATGAAACT 244
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      176 TAAACGTCACGTTGATTCATTACGCATGTTTACTCGTCTGCAACGAAAAAATT 235
QY      245 TCGTTGCTATGTCGAAAGCTTTAATAGAAAAAGATTTTCTTGTAATTGGTGGACT 304
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      236 TCGTTGCTATGTCAGAGGCTCTTATGCATACAGGTGATTTCTTATAATATAGTGCATT 295
QY      305 GGAAGAAAGGGTGCTGTGATGCTTTTGCTTCAACAAGAGATCTTGGGTTATTCCAAAG 364
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      296 GCGGATGGCTGCTGTGATGATGAATACCCAGGCTGAAGTATATGTTTATAAGGCTG 355
QY      365 CCGTTGAAACACACGTCACGTTGGAATAATTGTAAGCTGATTTTACAAAACTAATTGTAG 424
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB      356 CCGTGGTATATACACGCTTAGTTGGAATTTTATCGCTATGATCGCAAGAAACTGTAG 415
QY      425 AAAAATATAAAGTGCTGATATCAAAATATACGATTGATCGGGCATAGTTGGCGCCGATA 484
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      416 AACATATAAAGTGCCGATGACAAATATACGACTGTGGGACACAGATTGGCGCACACA 475
QY      485 CTTCAGGTTTTCGGGAAAGAGTTCAAAAGTTAAATTTAGAAAAATACAGGAATTA 544
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      476 TTTCAGGTTTCGACAGCAAAAGATTCAAGAGTTAAATTTAGAAAAATTTCTGAAATTA 535
QY      545 TCGGCTTGATCTGCTGACCGGTATTTTCATCGAGTGAAGTACTGTCGGACAGACTTGGCG 604
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      536 TTGGCTTGATCTGCTGGGCTTAGTTTCAAGAAAAATGATTGTTCCGAGAAATCTGCG 595
QY      605 TAACAGACGAGATAATGTTCAAGTTATACATACATCAATCATATTAGAGTATATTATA 664
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      596 AGACAGACGACATATGTAACAATTTTACATACATCGAAGCAATTTAGAACAGAGAGA 655
QY      665 ATGTTGCTAGCGTTGATTTCTACGTGATTAAGGAAAAATCAACCTGTTGC----- 717
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      656 CTCTTGGACACCGTCGATTTCTACATTAATTAACGGAAGTAATCAACCCGTTGCAGATATA 715
QY      718 --AATGAACCATCTGCTCTCATACGAAAGCCCGTGAATATCTGACTGAGTGCAATAAAC 775
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      716 TTATTTGAGAAACTTGCTCTCATACGAGACCGGTGAATACTTTACCGAGTGCAATAAGAC 775
QY      776 ATGAATGTTGTTAATTGGAACACCATGGAAGAAATATTTCAGCACTTCCAAAACCAATT 835
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      776 GCGAATGTTGTTAATTGGGGTCCC-----GCAGTCCAAGAAATCCGACCTGTTT 826
QY      836 CCCAGTCAGAGAGACACCTGTGTTTGCCTGATGTAATGCAAAAAAGTTATCCTGCTA 895
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      827 CGAAGTCACAGAAACAGAGTGCGTTTGCGTTGAATTAACGCAAGAAATATCCTAATA 886
QY      896 GAGGCCATTTTATGACACCGGTTGAAGCAAAATGCAACCTTATGCCATAACGAGGGATTA 955
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      887 GGGGCTCATTTTATGTACCGGTTGAAGCTGAAGCTGCATATTGCAATTAACAACGGGAAA 946
QY      956 AACTTTAATTATAAACAAGTCAATGTACACAAAAATGTATCTATTGTAATATTAA 1015
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      947 TAAATTAATTATATAAATAAACATTACTATTGACACAAGTGCAATTTGTTAATGATGAAA 1006
QY      1016 TGAATTAACGAACAGTCAATAATAAAAAAAAAAAAA 1048
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1007 TGAATTAATTACGATTCAGAAAAAATAAAAAA 1039

```

```

RESULT 4
US-08-385-745-16
: Sequence 16, Application US/08385745
: Patent No. 5612209
:
: GENERAL INFORMATION:
:
: APPLICANT: King, Te Piao
:
: TITLE OF INVENTION: Cloning and Recombinant Production of
:
: TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
:
: NUMBER OF SEQUENCES: 27
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: Pennie & Edmonds
:
: STREET: 1155 Avenue of the Americas
:
: CITY: New York
:
: STATE: New York
:
: COUNTRY: U.S.A.
:
: ZIP: 10036-2711
:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC compatible
:
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: PatentIn Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/08/385,745
:
: FILING DATE:
:
: CLASSIFICATION: 435

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/031,400
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 3288-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1050 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
US-08-385-745-16

Query Match 42.1%; Score 441; DB 1; Length 1050;
Best Local Similarity 67.0%; Pred. No. 4e-107;
Matches 665; Conservative 0; Mismatches 310; Indels 18; Gaps 2;

```
OY 65 CGGATTGCTTAAATGAGAAAGATATAGTATCTATGTTTACTCAAGGATAAGCGAG 124
DB 56 CCGTATGTCCTTATGATGATACAGTTAAGATGATTTTAAACAGGAAACCGAA 115
OY 125 ATGGTATATCTTAAGAAAGAACTTAAACGAATTACGATCTGTTTCAAAAGTCTACAA 184
DB 116 AACATGATTTTATACGCTAGATACATGAACAGGCACAATGAATTTAAGAAGTCAATCA 175
OY 185 TATCAAAAACAGTGTATTTCTTATACATGTTCTTCAACTGGAAATGAAGAACT 244
DB 176 TAAACGTCAGTGTATTCATTAACGATGTTTAACTTCTGTCGAACCGAAAAAAT 235
OY 245 TCGTTGCTATGCGAAAGCTTAAATAGAAAAAGATTTTCTGTAATTCGGTCACT 304
DB 236 TCGTTGCTATGTCAGAGGCTTATGATACAGGATTTCTTATATATATGTCGATT 295
OY 305 GGAAGAAGGGTGTGTTATGCTTTTCTTCAACAAAGATGCTTGGGTTATTCCAAAG 364
DB 296 GGGCGATGGCTGCTGTACTGATGAATACCCAGGCTGGAATATATGTTTATAAGGCTG 355
OY 365 CCGTTGGAACACACGTCAGTTGAAATTTGAGCTGATTTCACAAAATACTGTTAG 424
DB 356 CCGTTGTAATACACGCTTAGTTGAAATTTTATGCTATGATCGCAAGAAACTGTTAG 415
OY 425 AAAATATAAAGTGTGATATCAATATACGATGATCGGATAGTTGGGCGCGCAT 484
DB 416 AACATATAAAGTCCGATGACAAATATACGACTGGTGAGACACAGTTGGGCGCACACA 475
OY 485 CTTCAAGTTTTCGCGGAAAGAGTTCAAAAGTTAAATTAGAAAAATACAAGAAATTA 544
DB 476 TTTCAAGTTTTCGAGGCAAGAGATTCAAGAGTTAAATTAAGAAATTTCTGAATTA 535
OY 545 TCGGGCTTGATCTGCTGACCGGTATTTTCATCGAGTGAAGTCCGACAGACTTTGCG 604
DB 536 TTGGGCTTGATCTGCTGAGCCCTAGTTTCAAGAAAAATGATTTCCAGAGAAATCTGCG 595
OY 605 TAAACAGACGCAATATGTTCAAGTTATACATACATCAATCATATTAAGAGTATATTATA 664
DB 596 AGACAGACGCAATATGTTCAAAATTTTACATACATCGAGCAATTTAGGAAACAGAGAGAA 655
OY 665 ATGTTGTTAGCGTTGATTTCTACGTAATTATGAAAAAATCAACCTGCTGC----- 717
DB 656 CTCTTGGCACCGTGAATTTCTACATAAATTAACGAAAGTAAATCAACCCGTTGCAGATATA 715
OY 718 --AATGAACCATCTGCTCTATACGAAGCCGTGAATATATCTGACTGATGATTAAC 775
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DB 716 TTATTGAGAAACTGCTCTCATACGAGACCGGTGAATACTTTACCGAGTGCATAGAC 775
OY 776 ATGAATGTTGTTAATTTGAACACCATGGAAGAAATATTTACAGACTCCAAAACCAATTT 835
DB 776 GCGAATGTTGTTAATTTGGGGTCCC-----GCAGTCCAAAGAAATCCGACGCTGTTT 826
OY 836 CCCAGTGCAGAGAGACACCTGTGTTGGCTTGATTTGAATGCAAAAAGTTATCTGCTA 895
DB 827 CGAAGTGACACAGAAACGAGTGCCTTGGCTTGATTTAAACGCAAGAAATATCTTAA 886
OY 896 GAGGCGCATTTTATGACCCGGTTGAAGCAAAATGCACCTTATTTGCCATAACGAGGGATTA 955
DB 887 GGGGCTCATTTTATGTACCGGTTGAAGCTGAAGCTCCATATTTGCAATTAACACGGGAAA 946
OY 956 AACTTATATTAACAAAGTCAATGTACACAAAAATGTATCTATTTGATGATATTTAA 1015
DB 947 TAATTTAATTATTAATAAAAAACATTACTATTGACACAAAGTCAATTTGTTAATGATGAA 1006
OY 1016 TGAATTAACGACAGTCAATTAATAAAAAA 1048
DB 1007 TGAATTAATTAACGATTCAGAAAAA 1039
```

RESULT 5
US-08-485-388-16
Sequence 16, Application US/08485388
Patent No. 6270763
GENERAL INFORMATION:
APPLICANT: King, Te Piao
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,388
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/385,745
FILING DATE: 08-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/031,400
FILING DATE: 11-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 FWCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1050 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY:	CDS
LOCATION:	1..951
US-08-485-388-16	

Query Match	42.1%;	Score 441;	DB 3;	Length 1050;
Best Local Similarity	67.0%;	Pred. No. 4e-107;		
Matches 665; Conservative	0;	Mismatches 310;	Indels 18;	Gaps 2;

QY	65	CCGATTGCTACTTTTAATGAGAAAGATATAGTATTCTATGTTTAACTCAAGGGATAAGCGAG	124
Db	56	CCGTATGTCCCTTAGTAATGATACAGTTAAGATGATTTTAAACAAGGAAAAACCGAA	115
QY	125	ATGTATTATTCTTAAGAAAGAACTTTAACGAATTACGATCTGTTTACAAGTCTACAA	184
Db	116	AACATGATTTTATACGCTAGATACAATGACAGGCACAAATTAAGAAGTCAATCA	175
QY	185	TATCAAAACAAGTTGATTTCTTATACATGTTTCTTTCACCTGGGAATATGAAACT	244
Db	176	TAAACGTCACAGTTGTAATTCATTACGCATGGTTTACTTCGCTCGCAACCGAAAAAAT	235
QY	245	TGCTTGCTATGTCGAAAGCTTTAATAGAAAAAGTGAATTTTCTGTAAATTCGGTGCAC	304
Db	236	TGCTTGCTATGTCAGAGGCTCTTATGCATACAGGTGATTTCTTATTAATATGTCGATT	295
QY	305	GGAAGAAGGGCTGTTGTAATGCTTTTGCTTCAACAAGGATGCTTTGGGTTATTCGAAG	364
Db	296	GGCGGATGGCTGCTTGTAATGATGAATACCCAGGCTGGAATATATGTTTATTAAGGCTG	355
QY	365	CCGTTGAAACACACGTCACGTTGGAATAATTGTAAGTATTTTACAATACTACTTGTAG	424
Db	356	CCGTTGTAATACACGCTTAGTTGGAATAATTATCGCTATGATCGCAAGAAGAACTTGTAG	415
QY	425	AAAAATATAAGTCTGTAATCAATATATACGATTGATCGGCGATAGTTTGGCGCGCAT	484
Db	416	AACATATATAAGTCCGATGACAAATATACGATGCTGTGGGACACAGTTTGGCGCACACA	475
QY	485	CTTCAGGTTTGGCGGAAAAAGAGTTCAAAAGTTAAATTAAGAAAATCAAGGAATTA	544
Db	476	TTTCAGGTTTCCGACGGCAAAAGAGTTCAAGAGTTAAATTAAGAAAATTTCTGAAATTA	535
QY	545	TGCGGCTTGATCTGCTGGAACCGTATTTTCATCGAGTGACTGTCGGACAGACTTTGCG	604
Db	536	TTGGCTTGATCTGCTGCGGCTTAGTTTCAAGAAAAATGATTTGTTCCGAGAAATCTGCG	595
QY	605	TACAGACGCAAGTATGTTCAAGTTATACATACATCAATCATATTAGAGTATATTATTA	664
Db	596	AGACAGACGCAATATGTAACAATTTTACATACATCGAGCAATTTAGGAACAGAGAAA	655
QY	665	ATGTTGTAAGCTGTAATTTCTACGTAATATGGAATAATCAACCTGTTGC-----	717
Db	656	CTCTTGGAACCGTCAATTTCTACATAATTAACGGAAGTAATCAACCCGGTTGCAGATATA	715
QY	718	--AATGAACCATCTGCTCTCATACGAAAGCCGTGAAATATCTGACTGAGTGCATAAAA	775
Db	716	TTATTGAGAAACTGCTCTCATACGAGAGCCGTGAATACTTACCGAGTGCATTAAGAC	775
QY	776	ATGAATGTTGTTAAATGGAACAACCATGGAAGAAATATTGACACTCCAAAAACCAATT	835
Db	776	GCGAATGTTGTTAAATGGGGTCCC-----GCAGTCCAAGAAATCCGACGCTGTTT	826
QY	836	CCCAGTGCAGAGAGACACTGTGTTTGCCTTGATGATGCAAAAAAGTTATCTGCTA	895
Db	827	CGAAGTGCACAAGAAACGAGTGGCTTGGCTGATTAACGCAAGAATAATCTTAATA	886
QY	896	GAGGCGCATTTTATGCAACCGGTTGAAGCAATGCACTTATTTGCCATAACGAGGGGATTA	955
Db	887	GGGCTCATTTTATGTAACCGGTTGAAGCTGAAGCTCCATATTTGCAATTAACAACGGGAAA	946
QY	956	AACCTTAATTATTAACAACAAGTCAATGTACACAAAAATGTATCTATTGATGAATATTA	1015
Db	947	TAAATTAATTATTAATAAAAAACAATTACTATTGACACAGTGCAATTTGTTAATGATGAA	1006
QY	1016	TGAATTAACGAACAGTCAAAATTAATAAAAAA 1048	

Db 1007 TGATAAATACGATTCAGAAAAA 1039

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1      RESULT 6
2      US-08-474-853-16
3      ; Sequence 16, Application US/08474853
4      ; Patent No. 6287559
5      ; GENERAL INFORMATION:
6      ; APPLICANT: King, Te-piao
7      ; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
8      ; TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
9      ; TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
10     ; NUMBER OF SEQUENCES: 62
11     ; CORRESPONDENCE ADDRESS:
12     ; ADDRESSEE: Klauber & Jackson
13     ; STREET: 411 Hackensack Avenue
14     ; CITY: Hackensack
15     ; STATE: New Jersey
16     ; COUNTRY: USA
17     ; ZIP: 07601
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Floppy disk
20     ; COMPUTER: IBM PC compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/08/474,853
25     ; FILING DATE: 07-JUN-1995
26     ; CLASSIFICATION: 435
27     ; PRIOR APPLICATION DATA:
28     ; APPLICATION NUMBER: US 08/180,209
29     ; FILING DATE: 11-JAN-1994
30     ; PRIOR APPLICATION DATA:
31     ; APPLICATION NUMBER: US 08/031,400
32     ; FILING DATE: 11-MAR-1993
33     ; ATTORNEY/AGENT INFORMATION:
34     ; NAME: Jackson Esq., David A.
35     ; REGISTRATION NUMBER: 26,742
36     ; REFERENCE/DOCKET NUMBER: 600-1-074 CIPB
37     ; TELECOMMUNICATION INFORMATION:
38     ; TELEPHONE: 201 487-5800
39     ; TELEFAX: 201 343-1684
40     ; TELEX: 133521
41     ; INFORMATION FOR SEQ ID NO: 16:
42     ; SEQUENCE CHARACTERISTICS:
43     ; LENGTH: 1050 base pairs
44     ; TYPE: nucleic acid
45     ; STRANDEDNESS: single
46     ; TOPOLOGY: linear
47     ; MOLECULE TYPE: cDNA
48     ; FEATURE:
49     ; NAME/KEY: CDS
50     ; LOCATION: 1..951
51     ; US-08-474-853-16

```

[illegible]


```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/180,209B
; FILING DATE: 11-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/031,400
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-074 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1341 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 153..1052
; US-08-180-209B-26

```

```

Query Match 40.7%; Score 426.2; DB 1; Length 1341;
Best Local Similarity 66.9%; Pred. No. 3.7e-103;
Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;

```

```

QY 64 CCGATTGTACTTTTAATGAGAAAGATATAGTATCTATGTTTACTCAAGGATAAGCGA 123
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 156 CCAGATGTCTTTTAAATCTGATACAGATTGCGATAATATTGAACAGGAAACCGA 215
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 124 GATGATATATCTTAAAGAAAGAACTTTAAGCAATTAAGATCTGTTTACAAGTCTACA 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 216 AATCGTATCTTATACACTACAGACATTACAGAAATCATCTGAATTTAAGAAAAAACT 275
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 184 ATATCAAAACAGTGTATTTCTTATACATGTTTCTTCAACTGGGAATTAAGAAAC 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 276 ATACACAGTCCAGTGTATTCATTAACATGTTTACTCATCTGCAAGTGAACAAAT 335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 244 TTCGTTGCTATGTCGAAGCTTTAATAGAAAAAGATGATTTCTTGTAATTTCGTCGAC 303
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 336 TTCATTAATTTAGCAAAAGCTTTGGTAGATAAAGATACTATATGGTTATCTCAATCGAT 395
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 304 TGAAGAAGGGTGTGTAATGCTTTTGTCAACAAAGATGCTTTGGGTATTTCCAAA 363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 396 TGGCAGACGGCTGTGTAATAAGAGTCAAGGTTTAAAGTATTTATATATCTACT 455
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 364 GCGTTGGAACACACGTCAGTTGGAATTTAGCTGATTTTACAATACTACTTGT 423
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 456 GCTGCTAGAAATACAGTTAGTTGACAATATATCGTACGATTACCGAGAACTCGTA 515
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 424 GAAAAATATAAGTGTGATATCAATATATCAATGATCGGGCATAGTTGGCGCGCAT 483
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 516 AAACACTATAAATCTCGATGGCAATATATCAATTAATTGACATAGCTTAGAGACAT 575
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 484 ACTTCAGGTTTGGGGGAAAGAGTCAAAAGTTAAAATTAGGAAATAACAAGAAATT 543
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 576 GCTTCAGGTTTGGCAGGCAAAAAGTTCAAGAGTTAAAAATTAGGAAATAATTCTGAAATT 635
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 544 ATCGGGCTGATCTGTGGAACCGTATTTTCAATCGAGTGACTGTCCGACAGACTTTC 603
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 636 ATGGGGCTGATCTGTGAGCCCTTGTTCATTCATCAATCATTTGTCGAAAAGACTCTGC 695
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 604 GTAACAGACGCAAGATATGTTCAAGTTATACATCAATCATATTAGAGTATATTAT 663
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Db 696 GAGACAGATGACAAATATGTTCAAAATTATACATACATCAAACTATTAGAAACGAAAAA 755
QY 664 AATGTTGTAGCTGATTTCTACGTGAATTAAGAAAAAATCAACCTGTGCAATGAA 723
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 756 ACCCTTGTAACGTTTCTACATGAATAACGAAAGAAATCAACCTGTGCGTAGA 815
QY 724 CCATCC-----TGCTCTCATACGAAAGCCGTGAATATCTGACTGATGATATAAA 774
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 816 TTTTCTCAGAGATTGCTCTCATTCGAGGCCGTGATATACATGCTGAGTCAATAAA 875
QY 775 CATGAATGTTGTTAATTGGAACACCATGGAAGAAATATTTCAGCACTCCAAAACCAATT 834
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 876 CACGAATGTTGTTAATTGGGATACC-----GAAGTCAAGAGTTGCGACGCTTATT 926
QY 835 TCCCAAGTCAAGAGACACACCTGTGTTGGCTTGATTTGAATGCAAAAAAGTTATCTGCT 894
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 927 TCGTCGTGACAAACAGAGAGTGCCTTGGCTTGATTTAAACGCAAGAAAGTATACTAGT 986
QY 895 AGAGCGCATTTTATGCAACCGTTGAAGCAATGCACTTATTTGCCATTAACGAGGGGATT 954
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 987 AGAGGCTCATTTTATGTAACCGTTGAAGTACTGTTCTTTTGGCAATTAACAGGGGAAG 1046
QY 955 AAACCTTAATTAATAACAAAGTCAATGTACACAAAAATGTATGATGATGATATATA 1014
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1047 ATAATTTAATAATTAATAAAAGT-AAATTCATTCATCGAAATGCAATTTGTTAATGTGA 1105
QY 1015 ATGAATAAACGACGTCGAATAAAA 1041
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Db 1106 ATGAATAAATTACCAATTAACAAATAA 1132

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RESULT 10
US-08-385-745-26
; Sequence 26, Application US/08385745
; Patent No. 5612209

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; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: Vespil Venom Phospholipases, and Immunological Therapies
; TITLE OF INVENTION: Based Thereon
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,745
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/031,400
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 3288-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1341 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 153..1052
US-08-385-745-26

Query Match 40.7%; Score 426.2; DB 1; Length 1341;
Best Local Similarity 66.9%; Pred. No. 3.7e-103;
Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;

QY 64 CCGGATTGTAAGTTTAAATGAGAAAGATATAGTATCTATGTTTACTCAAGGGAATAAGCGA 123
DB 156 CCCAAATGTCCTTTTAAATCTGATACAGTTTCGATAATTAATGAACAGGGAACCGA 215
QY 124 GATGTAATTAATCTTAAGAAAGAACTTTAAGCAATTCAGATCTGTTACAAAGTCTACA 183
DB 216 AATCGTATCTTATACACTACAGACATTACAGAATCATCTGAATTTAAGAAAAAACT 275
QY 184 ATATCAAAACAAGTTGATTTCTTATACATGTTCTTCAACTGGGAATATGAAAC 243
DB 276 ATAACAGTCCAGTTGATTAATTAACATAGTTTACTTCACTGCAAGTGAAACAAAT 335
QY 244 TTCGTTCTATGTCGAAAGCTTTAATAGAAAAAGATGATTTCTTGAATTTGGTCGAC 303
DB 336 TTCATTAATTTAGCAAAAGCTTGTAGATAAGATACTATATGTTATCTCAATCGAT 395
QY 304 TGGAGAAGGGTCTGTTGATGCTTTTGCTTCAACAAGATGCTTTGGTTATTCGAAA 363
DB 396 TGGCAGAGCGCTGCTGTACTATGAAAGTCGAGGTTAAAGTATTATATATCTCTACT 455
QY 364 GCCGTGGAACACACGTCACGTTGAAAAATTTGATGATTTTACAAAACACTTGTGA 423
DB 456 GCTGCTAGAAATACACGTTTGTGACCAATATATCGCTACGATTAACCAAGAACTCGTA 515
QY 424 GAAAAATATAAGTGCTGATATCAATATACGATTGATCGGGCATAGTTGGGCGGCAT 483
DB 516 AAACACTATAAATCTCGATGGCAATATACGATTAAATTTGACATAGCTTAGAGACACAT 575
QY 484 ACTTCAGGTTTTCGGGAAAGAGTTCAAAAGTTAAATTTAGAAAAATACAGAAAT 543
DB 576 GCTTCAGGTTTTCAGGCAAAAGTTCAAGAGTTAAATTTAGAAAAATATCTGAAAT 635
QY 544 ATCGGCTTGATCCCTGCTGACCGTATTTTCATCGGAGTGAATGTCGAGACACTTTGC 603
DB 636 ATTGGCTTGATCCCTGCTAGGCTTCGTTGATTCAAATCATGTTCCGAAAGACTCTGC 695
QY 604 GTAACAGACGCAAGATATGTTCAAGTTATACATACATCAATCATATTAGAGTATATT 663
DB 696 GAGACAGATGCAGAAATATGTTCAAAATTAATACATACATCAAACTATTAGGAACGAAAA 755
QY 664 AATGTTGTAAGCGTTGATTTCTACGTAATTATGAAAAAATCAACCTGTTGCAATGAA 723
DB 756 ACCCTTGTAACCGTGAATTTCTACATGAATAACGAAAGAAATCAACCTGTTGCGGTAGA 815
QY 724 CCATCC-----TGCTTCATACGAAAGCCGTGAATATCTGACTGAGTCATAAAA 774
DB 816 TTTTCTCAGAAAGTTTGTCTCTCATTCGAGAGCCGTGATATACATGCTGAGTCATAAAA 875
QY 775 CATGATGTTGTTAATTTGAACCATGGAAGAAATTTTCAGCACTCCAAACCAATT 834
DB 876 CACGAATGTTGTTAATTTGGATACC-----GAAGTCAAAAGAGTTCCGACGCTATT 926
QY 835 TCCCAAGTCAAGAGACACCTGTGTTTGGTTGGATGATGCAAAAAAGTATCTCTGCT 894
DB 927 TCGTCGTGACAAAAACAGAGTGGCTTGGCTGATTAACGCAAGAGATATACTAGT 986
QY 895 AGAGGCGATTTTATGCAACCGGTTGAAGCAATGCACTTATGCCATTAACGAGGGGATT 954
DB 987 AGAGGCTCATTTTATGTAACCGGTTGAAAGTACTGTTCTTTTTCGAATTAACAGGGGAG 1046
QY 955 AAACTTTAATTAATAACAAAGTCAATGTACACAAAAATGTATCTATTGATGATATTAA 1014

DB 1047 ATAAATTAATAATATAAAAAAGT-AATTTCCATTCATCGAAATGCAATTTGTTAATGTGA 1105
QY 1015 ATGAATAAACGACAGTCAATAAAAA 1041
DB 1106 ATGAATAAATTACCATTTTAACAAATAA 1132

RESULT 11
US-08-485-388-26
Sequence 26, Application US/08485388
Patent No. 6270763
GENERAL INFORMATION:
APPLICANT: King, Te Piao
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
TITLE OF INVENTION: Based Thereon
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,388
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/385,745
FILING DATE: 08-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/031,400
FILING DATE: 11-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 FWCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 153..1052
US-08-485-388-26

Query Match 40.7%; Score 426.2; DB 3; Length 1341;
Best Local Similarity 66.9%; Pred. No. 3.7e-103;
Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;

QY 64 CCGGATTGTAAGTTTAAATGAGAAAGATATAGTATCTATGTTTACTCAAGGGAATAAGCGA 123
DB 156 CCCAAATGTCCTTTTAAATCTGATACAGTTTCGATAATTAATTTGAACAGGGAACCGA 215
QY 124 GATGTAATTAATCTTAAGAAAGAACTTTAAGCAATTCAGATCTGTTTACAAAGTCTACA 183
DB 216 AATCGTATCTTATACACTACAGACATTACAGAATCATCTGAATTTAAGAAAAAACT 275

QY 184 ATATCAAAACAAGTGTATTTCTTATACATGTTTCTTCAACTGGGAATAATGAAAC 243
 DB 276 ATAAACAGTCAGTGTATTCATACACATGTTTAACTTCATCTGCAAGTGAACAAT 335
 QY 244 TTCGTTGCTATGTCGAAAGCTTTAATAGAAAAAGATGATTTTCTGTAATTCGTCGAC 303
 DB 336 TTCATTAATTTAGCAAAAGCTTTGGTAGATAAGATACTATATGTTATCTCAATCGAT 395
 QY 304 TGGAGAAGGGTGTCTGTAATGCTTTTGTCTCAACAAGATGCTTTGGTTATTCCAA 363
 DB 396 TGGCAGACGGCTGCTGTACTAATGAAGTCGAGTTTAAAGTATTTATATCTACT 455
 QY 364 GCCGTTGGAACACACGTCAGTTGGAATTTGACCTGATTTTACAAACTACTGTA 423
 DB 456 GCTGCTAGAAATACACGTTAGTTGACACATATATCGCTACGATTAACCAAGAACTCGTA 515
 QY 424 GAAAAATATAAGTGTGATATCAATATACGATGATCGGGCATAGTTGGCCGCAT 483
 DB 516 AAACACTATAAATCTCGATGGCAAAATATACGATTAATTGACATAGCTTAGAGACACAT 575
 QY 484 ACTTCAGGTTTTCGGGAAAAAGATTCAAAAGTTAAATTAGAAAAATACAAGAAATT 543
 DB 576 GCTTCAGGTTTTCAGGCAAAAGTTCAAGAGTTAAATTAGAAAAATATCTGAATTT 635
 QY 544 ATCGGCTTGTATCTGCTGTCGACCGTATTTTCATCGAGTGACTGTCCGGACAGACTTGC 603
 DB 636 ATGGGCTTGATCTGCTGAGCCCTTCGTCGATCAATCATTTGTCGAAAGACTCTGC 695
 QY 604 GTAACAGACGCAATATGTTCAAGTTATACATATACATCATATATAGAGATATATAT 663
 DB 696 GAGACAGATGCAGATATGTTCAATTTATACATACATCAAACTATTTAGGAACCGAAAA 755
 QY 664 AATGTTGTAAGCTGTGATTTCTACGTAATTATGAAAAAATCAACCTGTTGCAATGAA 723
 DB 756 ACCCTTGTACCGTCGATTTCTACATGAATACGGAAGAAATCAACCTGTTGCGGTAGA 815
 QY 724 CCAATCC-----TGCTCTCATACGAAAGCCGTGAATATCTGACTGAGTCATAAAA 774
 DB 816 TTTTCTCAGAAAGTTGCTCTCATTCGAGAGCCGTGATATACATGCTGAGTCATAAAA 875
 QY 775 CATGAATGTTGTTAATGGAACACCATGGAAGAAATATTTCAACACTCCAAAACCAATT 834
 DB 876 CAGGAATGTTGTTAATGCGATACC-----GAAGTCAAGAGTTGCGACGCTATT 926
 QY 835 TCCAGTGACAGAGACACCTGTGTTGCGTTGATGATGCAAAAAAGTTATCTCTGCT 894
 DB 927 TCGTCGTGACAAAAACAGAGTGCCTTTCGTTGATTAACGCAAGAAAGTATACTACT 986
 QY 895 AGAGCGCATTTTATGCAACCGGTGGAAGCAATGCACTTATGCCATTAACGAGGGATT 954
 DB 987 AGAGGCTCATTTTATGTAACCGGTGGAAGTACTGTTCTTTTGCAATTAACAGGGGAAG 1046
 QY 955 AAACCTTAATTAATAACAAAGTCAATGTACAAAAATGTATCTATGATGATATTTAA 1014
 DB 1047 ATAAATTAATTAATAAAAAAGT-AAATTCATTCATCGAAATGCAATTTGTTATGTTGA 1105
 QY 1015 ATGAATAAACGACAGTCATAATAAAA 1041
 DB 1106 ATGAATAAATTACCATTTTAACAAAATAA 1132

RESULT 12
 US-08-474-853-26
 ; Sequence 26, Application US/08474853
 ; Patent No. 6287559
 ; GENERAL INFORMATION:
 ; APPLICANT: King, Te-Piao
 ; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
 ; TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
 ; TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
 ; NUMBER OF SEQUENCES: 62
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,853
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/180,209
 FILING DATE: 11-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/031,400
 FILING DATE: 11-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-074 CIPB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEFAX: 201 343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1341 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 153..1052
 US-08-474-853-26

Query Match 40.7%; Score 426.2; DB 3; Length 1341;
 Best Local Similarity 66.9%; Pred. No. 3.7e-103;
 Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;
 QY 64 CCGATTGTACTTTAATGAGAAAGATATGATTTCTATGTTTACTCAAGGATAGCGA 123
 DB 156 CCCAATGTCCTTTAATTTCTGATACAGTTTCGATATATTTAGAAACAGGAAACCGA 215
 QY 124 GATGCTATTTCTTAAGAAAGAACTTTAAGCAATTCGATCTGTTTACAAAGCTTACA 183
 DB 216 AATCGTATCTTTATACACTACAGACATTAAGAAATCATCTGAAATTTAAGAAAAAACT 275
 QY 184 ATATCAAAACAAGTGTATTTCTTATACATGTTTCTTCAACTGGGAATTAATGAAAA 243
 DB 276 ATAAACAGTCAGTTGTATTCAATTACATGATGTTTACTTCAATCTGCAAGTGAACAAAT 335
 QY 244 TTCGTTGCTATGTCGAAAGCTTTAATAGAAAAAGATGATTTTCTGTAATTCGTCGAC 303
 DB 336 TTCATTAATTTAGCAAAAGCTTTGGTAGATAAGATACTATATGTTATCTCAATCGAT 395
 QY 304 TGGAGAAGGGTGTCTGTAATGCTTTTGTCTTCAACAAGATGCTTTGGTTATTCCAA 363
 DB 396 TGGCAGACGGCTGCTGTACTAATGAAGTCGAGTTTAAAGTATTTATATCTACTACT 455
 QY 364 GCCGTTGGAACACACGTCACGTTGGAATTTGACCTGATTTTACAAACTACTGTA 423
 DB 456 GCTGCTAGAAATACACGTTAGTTGACACATATATCGCTACGATTAACCAAGAACTCGTA 515
 QY 424 GAAAAATATAAGTGTGATATCAATATACGATGATCGGGCATAGTTGGCCGCAT 483
 DB 516 AAACACTATAAATCTCGATGGCAAAATATACGATTAATTGACATAGCTTAGAGACACAT 575
 QY 484 ACTTCAGGTTTTCGGGAAAAAGAGTTCAAAAGTTAAATTAGAAAAATACAGAAATTT 543

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Db      576 GCTTCAGGTTTTCAGCGCAAAAAGTTCAAGAGTTAAATTAAGAAAATATTCTGAATT 635
Qy      544 ATCGGGCTTGATCCTGCTGACCGTAATTTTCATCGAGTGACTGTCGGACAGACTTTGC 603
Db      636 ATGGGCTTGATCCTGCTAGCGCTTGCTGATTCAAAATCATTTGTTCCGAAGACTCTGC 695
Qy      604 GTAACAGACGAGATATGTTCAAGTTATACATACATCAATCATATTAGAGTATATTAT 663
Db      696 GAGACAGATGCAAGATATGTTCAAAATTATACATACATCAAACTATTAGGAACGAAAA 755
Qy      664 AATGTTGTAAGCTTGATTTCTACGTGAATTATGAAAAAATCAACCTGGTTGCAATGAA 723
Db      756 ACCCTTGGTACCGTCGATTCTACATGAATTAACGAAAGAAATCAACCTGGTTGCGGTAGA 815
Qy      724 CCATCC-----TGCTCTCATACGAAAAGCCGTGAATATCTGACTGAGTGCATAAAA 774
Db      816 TTTTCTCAGAAAGTTTGCTCTCATTCGAGAGCCGTGATATACATGGCTGAGTGCATAAAA 875
Qy      775 CATGAATGTTGTTAATTGGAACACCATGGAAGAAATATTTCAGCACTCCAAAACCAATT 834
Db      876 CACGAATGTTGTTAATTGGGATACC-----GAAGTCAAAAGATTGCGACGCTATT 926
Qy      835 TCCCAATGACAGAGACACCTGTGTTGCGTTGATTGAATGCAAAAAAGTTATCCTGCT 894
Db      927 TCGTGTGCACAAAACAGAGTGCCTGTTGCGTTGATTAAACGCAAGAAGTATATCTAGT 986
Qy      895 AGAGGCGCATTTTATGCACCCGTTGAACCAATGCACCTTATGCCATAACGAGGGGATT 954
Db      987 AGAGGCTCATTTTATGTACCCGTTGAAGTACTGTTCCTTTTTGCAATTAACAGGGGAAAG 1046
Qy      955 AAACCTTAATTATTAACAAAAGTCAATGTACACAAAATGTATCTATTGATGAATATTAA 1014
Db      1047 ATAATTTAATTAATATAAAAAAGT-AAATTCATTCAATCGAAATGCATTGTTAATGGTGA 1105
Qy      1015 ATGAATTAACGAACAGTCAAAATAAAA 1041
Db      1106 ATGAATTAATTAACATTTAACAAATTA 1132
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RESULT 13
US-09-166-205B-26
; Sequence 26, Application US/09166205B
; Patent No. 6372471
; GENERAL INFORMATION:
; APPLICANT: Te Piao KING
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES,
; TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL
; TITLE OF INVENTION: THERAPIES BASED THEREON
; FILE REFERENCE: 2313/0F138US
; CURRENT APPLICATION NUMBER: US/09/166,205B
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Vesputia vulgaris
US-09-166-205B-26
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Query Match      40.7%; Score 426.2; DB 3; Length 1341;
Best Local Similarity 66.9%; Pred. No. 3.7e-103;
Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;

Qy      64 CCGATGTACTTTTAATGAGAAAGATATAGTATTCTATTGTTTACTCAAGGATTAAGCGA 123
Db      156 CCCAAATGTCCTTTTAATTCGTATACAGTTTCGATTAATTAATGAAACAGGAAAAACGA 215
Qy      124 GATGTTATTTCTTAAGAAAGAACTTTAAGCAATTAAGATCTGTTTACAAAGTCTACA 183
Db      216 AATCGTATCTTTATACACTACAGACATTACAGAATCATCTGAATTTAAGAAAAAACT 275
Qy      184 ATATCAAAACAAGTTGTATTCTTATACATGTTTCTTTCAACTGGAATATGAAAC 243
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Db      276 ATACACGTCAGTTGTTATTCATTAACACATGTTTATCTTCATCTGCAAGTGAAACAAAT 335
Qy      244 TTCGTTGCTATGTCGAAAGCTTTAATAGAAAAAGATGATTTTCTGTAATTTCCGTGAC 303
Db      336 TTCATTAATTTAGCAAAAGCTTTGGTAGATAAAGATATATATGTTATCTCATTCGAT 395
Qy      304 TGAAGAAGGCTGCTTGTATGCTTTTGCTTCAACAAAGATGCTTTGGTATTTCCAA 363
Db      396 TGGCAGACGCGCTGCTGTACTAATGAAGCTGCAGGTTTAAAGTATTATATTATTCCTACT 455
Qy      364 GCCGTTGGAACAACACGTCACGTTGGAATAATTGTAAGCTGATTTTACAAAACACTTCTGA 423
Db      456 GCTGCTAGAAATACACGTTTACTGGAATATATATCGCTACGATTACCCAGAAACTCTGTA 515
Qy      424 GAAAAATATAAGTGTGATATCAAAATATACGATTGATCGGGCATAGTTGGCGCGCAT 483
Db      516 AAACACTATAAAATCTCGATGCAAAATATACGATTAAATGGAACATAGCTTAGAGACAT 575
Qy      484 ACTTCAGTTTTCGCGGAAAAGATTCAAAAGTTAAATTAAGAAATATACAAAGAAATT 543
Db      576 GCTTCAGGTTTTCAGGCAAAAAGTTCAAGAGTTAAATTAAGAAATATTTCTGAATTT 635
Qy      544 ATCGGCTTGATCCTGCTGACCGGATTTTTCATCGAGTGACTGTCCGACAGACTTGC 603
Db      636 ATGGGCTTGATCCTGCTAGCGCTTCGTTGATTCAATCATTTGTTCCGAAGACTCTGC 695
Qy      604 GTAACAGACGCAAGATATGTTCAAGTTATACATACATCAATCATATTAGAGTATATTAT 663
Db      696 GAGACAGATGCAAGATATGTTCAAAATTATACATACATCAAACTATTTAGAACCGAAAA 755
Qy      664 AATGTTGTAGCGTTGATTCTACGTGAATTATGAAAAAATCAACCTGGTTGCAATGAA 723
Db      756 ACCCTTGTACCGTCGATTCTACATGAATTAACGAAAGAAATCAACCTGGTTGCGGTAGA 815
Qy      724 CCATCC-----TGCTCTCATACGAAAAGCCGTGAATATCTGACTGAGTGCATAAAA 774
Db      816 TTTTCTCAGAAAGTTTGCTCTCATTCGAGAGCCGTGATATACATGGCTGAGTGCATAAAA 875
Qy      775 CATGAATGTTGTTAATTGGAACACCATGGAAGAAATATTTCAGCACTCCAAAACCAATT 834
Db      876 CACGAATGTTGTTAATTGGGATACC-----GAAGTCAAAAGATTGCGACGCTATT 926
Qy      835 TCCCAATGACAGAGACACCTGTGTTGCGTTGATTGAATGCAAAAAAGTTATCCTGCT 894
Db      927 TCGTGTGCACAAAACAGAGTGCCTTTGCGTTGATTAAACGCAAGAAGTATATCTAGT 986
Qy      895 AGAGGCGCATTTTATGCACCCGTTGAAGCAAAATGCACCTTATGCCATAACGAGGGGATT 954
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Db      1106 ATGAATTAATTAACATTTAACAAATTA 1132
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PCT-US94-02629-26
; Sequence 26, Application PC/TUS9402629
; GENERAL INFORMATION:
; APPLICANT: King, Te-Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
; TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
```

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STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02629
FILING DATE: 10-MAR-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/180,209
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,400
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEO ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 153..1052
PCT-US94-02629-26
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Query Match 40.7%; Score 426.2; DB 5; Length 1341;
Best Local Similarity 66.9%; Pred. No. 3.7e-103;
Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;
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QY 244 TTCGTTGCTATGTCGAAAGCTTTAATAGAAAAAGATGATTTCTTGAATTCGTCGAC 303
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QY 364 GCCGTTGGAACACAGCTCAGCTTGAAAAATTTAGCTGATTTTACAACACTACTGTA 423
Db 456 GCTGCTAGAAATACAGCTTAGTGAACAATATCCCTACGATTACCCAGAAACTCGTA 515
QY 424 GAAAAATATAAGTGTGATATCAATATACGATGATCGGCAATAGTTGGCGCGCAT 483
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Db 1106 ATGAATAAATTACCATTTAACAATAAA 1132
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RESULT 15
US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAB1 promoters
US-09-806-708B-22
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Query Match 5.6%; Score 59; DB 4; Length 1141;
Best Local Similarity 12.5%; Pred. No. 8.8e-06;
Matches 131; Conservative 357; Mismatches 552; Indels 5; Gaps 2;
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QY 61 TCTCCGATTTGTAATTTAATGAGAAAGATATAGTATTCTATGTTTACTCAAGGAGTAAG 120
Db 151 TMCMDKDKRTRVWWKNNNATGWDJTKYHMMNNNGCBTVTWVRYKTDSDWSBKMN 210
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QY 361 AAAGCCGTTGGAACACACAGTCACGTTGGAATAATTGAGCTGATTTTACAAACTACTT 420
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QY 481 CATACCTCAGGTTTTCGCGGAAAGAGTTCAAAAGTTAAATTAGGAAATACAAAGAA 540
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QY 721 GAACCATCTGCTCTCATACGAAGCGCTGAATATCTGACTGAGTCATAAACAATGAA 780
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Db 1106 WHMCKCNNNNNNNTMRRAMAMAAA 1130
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Job time : 228 sec8

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2005, 21:42:49 ; Search time 731 Seconds
(without alignments)
8727.627 Million cell updates/sec

Title: US-10-688-011-1

Perfect score: 1048

Sequence: 1 atttgcttctgttagatga.....agtcataataaaaaaa 1048

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	1048	18	US-10-688-011-1
2	49.2	4.7	460	9	US-09-960-352-12840
3	48.6	4.6	3673778	16	US-10-312-841-1
4	47	4.5	3564	19	US-10-741-600-478
5	46.8	4.5	1526	17	US-10-398-663-12
6	46.8	4.5	3635	14	US-10-116-802-28
7	46.2	4.4	13326	15	US-10-311-455-1686
8	45.8	4.4	7786	9	US-09-790-988-2
9	45.6	4.4	1605	9	US-09-917-800A-1549
10	45.2	4.3	1383	17	US-10-312-088-1
11	45.2	4.3	1401	16	US-10-403-745-2

12	45.2	4.3	1404	13	US-10-038-517-1	Sequence 1, Appli
13	45.2	4.3	2352	16	US-10-403-745-1	Sequence 1, Appli
14	45.2	4.3	3549	9	US-09-954-456-2217	Sequence 2217, Ap
15	45.2	4.3	3549	10	US-09-802-640-13	Sequence 13, Appli
16	45.2	4.3	3549	17	US-10-403-902A-13	Sequence 13, Appli
17	45.2	4.3	3549	18	US-10-755-889-99	Sequence 99, Appli
18	45.2	4.3	3549	18	US-10-789-378-47	Sequence 47, Appli
19	45.2	4.3	3549	19	US-10-843-641A-5244	Sequence 5244, Ap
20	45.2	4.3	4075	10	US-09-971-392-107	Sequence 107, App
21	45.2	4.3	4314	18	US-10-723-860-6562	Sequence 6562, App
22	45	4.3	3184	9	US-09-934-268-1	Sequence 1, Appli
23	45	4.3	3184	14	US-10-162-435-35	Sequence 35, Appli
24	45	4.3	3184	19	US-10-860-779-35	Sequence 35, Appli
25	44.6	4.3	17294	15	US-10-311-455-960	Sequence 960, App
26	44.4	4.2	421	9	US-09-960-352-8123	Sequence 8123, Ap
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29	44.4	4.2	1603	17	US-10-403-902A-19	Sequence 19, Appli
30	44.4	4.2	1603	18	US-10-335-053-235	Sequence 235, App
31	44.2	4.2	1767	16	US-10-349-680-163	Sequence 163, App
32	44.2	4.2	8634	15	US-10-311-455-1029	Sequence 1029, Ap
33	44.2	4.2	17389	15	US-10-311-455-1387	Sequence 1387, Ap
34	44	4.2	333	18	US-10-357-930-12856	Sequence 12856, A
35	43.8	4.2	16688	15	US-10-311-455-294	Sequence 294, App
36	43.6	4.2	433	18	US-10-425-115-12621	Sequence 12621, A
37	43.6	4.2	14112	15	US-10-311-455-1416	Sequence 1416, Ap
38	43.6	4.2	14112	17	US-10-221-714A-200	Sequence 200, App
39	43.6	4.2	14112	18	US-10-433-793-10	Sequence 10, Appli
40	43.4	4.1	5857	15	US-10-311-455-502	Sequence 502, App
41	43.2	4.1	481	18	US-10-437-963-78790	Sequence 78790, A
42	43.2	4.1	1530	19	US-10-741-600-750	Sequence 750, App
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44	43.2	4.1	1975	18	US-10-425-115-80851	Sequence 80851, A
45	43.2	4.1	6109	15	US-10-311-455-299	Sequence 299, App

ALIGNMENTS

RESULT 1
US-10-688-011-1
; Sequence 1, Application US/10688011
; Publication No. US20040175393A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF POLISTINAE VENOM ENZYMES,
; TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL
; TITLE OF INVENTION: THERAPIES BASED THEREON
; FILE REFERENCE: 02313/100F138-US2
; CURRENT APPLICATION NUMBER: US/10/688, 011
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 09/806, 658
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US99/23211
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 09/166, 205
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Polistes annularis
US-10-688-011-1

Query Match 100.0%; Score 1048; DB 18; Length 1048;
Best local Similarity 100.0%; Pred. No. 1.6e-234;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTTCTGTAGATGATTCGACGACATTTAGAAATGTACCTTGAATGAGGCATG 60
Db 1 ATTGCTTCTGTAGATGATTCGACGACATTTAGAAATGTACCTTGAATGAGGCATG 60

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Db 121 CGAGATGATATTATCTTAAGAAAGAACTTAAACGATTAACGATCTGTTTCAAAAGTCT 180
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RESULT 2
US-09-960-352-12840
; Sequence 12840, Application US/09960352
; Patent No. US20020137139A1

; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 12840
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 55-LIB2809-014-Q1-E1-F4
US-09-960-352-12840

Query Match 4.7%; Score 49.2; DB 9; Length 460;
Best Local Similarity 51.4%; Pred. No. 0.25;
Matches 148; Conservative 0; Mismatches 128; Indels 12; Gaps 1;
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Db 3 CCAAGCCCGCGGATACCAACCAAGCTGTGGACAGATGTGCCAAGTTATGAACTGA 62
QY 419 TTGTAGAAAAATATAAGTGTGATATCAAAATATACGATTCGGCATAGTTGGCG 478
Db 63 TGGCGGATGAATTTAATCTATCCCTGGGCAATGTGATCTCTTGGATACAGCCTTGGG 122
QY 479 CGCATACTTCAGGTTTTCGGGAAAAAGAGTTCAAAAAGTTAAATTAGGAAATACAAAG 538
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Db 171 GATTAACCGGCTTAGATCCAGCTGACCTTAACCTTGAGTATGCAAGAGCTCCAAGTCGCC 230
QY 599 TTGCGTAACAGACGACGAATATGTTCAAGTTATACATCATCAATCA 646
Db 231 TTCTCTGATGATGCGGATTTTGTAGACGTTTACACACATTCACCA 278

RESULT 3
US-10-312-841-1/c
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

Query Match 4.6%; Score 48.6; DB 16; Length 3673778;
Best Local Similarity 54.9%; Pred. No. 21;
Matches 96; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 874 AATGCAAAAAGTTATCTGCTAGAGGCGCATTTTATGACCGGTTGAAGCAAAATGACACT 933
Db 3246566 AAAATAAAATTTAATAACCTTAACAATCAATTTCTATCCCACTAAATCATAAACAAA 3246507

[illegible]

RESULT 4

```

; Sequence 478, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 3564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(3564)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-478

```

Query Match

Query Match	4.5%	Score 47;	DB 19;	Length 3564;
Best Local Similarity	50.7%;	Pred. No. 2.1;		
Matches 144;	Conservative	1;	Mismatches 127;	Indels 12;
				Gaps 1;

[illegible]

RESULT 5

```

US-10-398-663-12
; Sequence 12, Application US/10398663
; Publication No. US20040053281A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE, CORPORATION; HARLAND, Lee
; APPLICANT: ARVIZU, Chandra S.; DAS, Debopri
; APPLICANT: GRIEFIN, Jennifer A.; BAUGHN, Ma
; APPLICANT: DING, Li; CHAWLA, Narinder K.;
; APPLICANT: YAO, Monique G.; LU, Yan;
; APPLICANT: ELLIOTT, Vicki S.; THANGAVELU, K
; APPLICANT: RAMKUMAR, Jayalaxmi; LAL, Preeti
; APPLICANT: TRIBOULEY, Catherine M.
; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
; FILE REFERENCE: PI-0250 USN
; CURRENT APPLICATION NUMBER: US/10/398,663

```

```

: CURRENT FILING DATE: 2003-03-04
: PRIOR APPLICATION NUMBER: PCT/US01/31302
: PRIOR FILING DATE: 2001-10-05
: PRIOR APPLICATION NUMBER: US 60/238,388
: PRIOR FILING DATE: 2000-10-06
: PRIOR APPLICATION NUMBER: US 60/240,616
: PRIOR FILING DATE: 2000-10-13
: PRIOR APPLICATION NUMBER: US 60/245,719
: PRIOR FILING DATE: 2000-11-02
: PRIOR APPLICATION NUMBER: US 60/247,503
: PRIOR FILING DATE: 2000-11-08
: PRIOR APPLICATION NUMBER: US 60/249,503
: PRIOR FILING DATE: 2000-11-17
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PERL Program
: SEQ ID NO 12
: LENGTH: 1526
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No. US20040053281A1 7482937CB1
US-10-398-663-12

```

Query Match

Query Match	4.5%;	Score 46.8;	DB 17;	Length 1526;
Best Local Similarity	49.7%;	Pred. No. 1.6;		
Matches 160;	Conservative 0;	Mismatches 147;	Indels 15;	Gaps 1;

QY 318 TTGTAATGCTTTTGGCTTCAACAAGGATGCTTTGGGTTATTTCCAAAGCCGTTGGAACAC 377
Db 312 TTGCATTAAATTGATTTGATGATCAACGGTTCAACGGGGATACATCCATGCTGTAAACAATCT 371
QY 378 ACGTCACGTTGGAAAAATTGTAGCTGATTTTACAAAACCTACTGTAGAAAAATATATAAGT 437
Db 372 CCGTGTGTGTGGTCTGAGGTGGCTATTTATTGATGTTCATGAAAAAATTGTAATA 431
QY 438 GCTGATATCAATATATACGATTGATCGGGCATAGTTTGGCGGCATACTTCAGGTTTTC 497
Db 432 TTCCCTCTCTAAAGTGACCTGATTGGCCACAGCTTGGAGCACACCTGCTGGGGAAC 491
QY 498 GGGAAAAAGAAAGTTCAAAAGTTAAATTAGGAAATACAGAAATTTACGGGCTTGATCC 557
Db 492 TGG-----GTCAAGATACCAGGCCTTGGAAGAATACTGGGTTGGAACC 536
QY 558 TGCTGACCCGTAATTTTCATCGGAGTGACTGTCCGGACAGACTTTGCGTAACAGACGCAGA 617
Db 537 AGCTGGGCCATTTTTCACACAACCTCCAAAAGAGTCAAGCCTAGACCCCTCGGATGCCAA 596
QY 618 ATAATGTTCAAGTTATACATACA 639
Db 597 CTTTGTGACGTTATTCATACA 618

9

```

US-10-116-802-28
; Sequence 28, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Lasек
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 3635
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature

```


OTHER INFORMATION: Incyte ID No: 3950154CBI
US-10-116-802-28

Query Match 4.5%; Score 46.8; DB 14; Length 3635;
Best Local Similarity 51.1%; Pred. No. 2.3;
Matches 145; Conservative 0; Mismatches 127; Indels 12; Gaps 1;

QY 365 CCGTTGGAACACACGCTGACGTTGGAAATTTGTAGCTGATTTTACAAACTACTGTAG 424
DB 620 CCGCGGGCTACACCAAACTGGTGGACAGAGATGGCCCGGTTTATCACTGGATGAGG 679
QY 425 AAAAATATTAAGTCTGATATCAATATACGATTGATCGGCGATAGTTGGCGCGCAT 484
DB 680 AGGAATTTAACTACCTCTGGAACAATGTCATCTCTGGATACAGCCTTGGAGCCCATG 739
QY 485 CTTCAGGTTTTCGGGAAAAAGTTCAAAAGTTAAATTAGGAAATACAAAGAAATTA 544
DB 740 CTGCTGGCATTGCAGAAAGTCTGACCAATAG-----AAAGTCAACAGAAATTA 787
QY 545 TCGGGCTTGATCCTGCTGACCGTATTTTCATCGGAGTGACTGTCCGACAGACTTTGCG 604
DB 788 CTGGCCCTCGATCCAGCTGACCTTACTTTGAGTATGCAAGAGCCCGAGTCTTCTTC 847
QY 605 TAAACAGACGAGATATGTTCAAGTTATACATACATCAATCATA 648
DB 848 CTGATGATGCAGATTTTGTAGACGCTTACACACATTCACCAGA 891

RESULT 7

US-10-311-455-1686
; Sequence 1686, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1686
; LENGTH: 13326
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1686

Query Match 4.4%; Score 46.2; DB 15; Length 13326;
Best Local Similarity 46.7%; Pred. No. 5.8;
Matches 191; Conservative 0; Mismatches 208; Indels 10; Gaps 1;

QY 66 GGATGTACTTTTAATGAGAAAGATATAGTATCTATGTTTACTCAAGGATAAGCGAGA 125
DB 12913 GGAATATTAAATTTTAAGTTAAGTATAGAAATATTTTATTATTACGAGATATTTTATG 12972
QY 126 TGGTATTATCTTAAGAAAGAACTTTAAGCAATTACGATCTGTTTACAAGTCTACAAT 185
DB 12973 TTGTTTATTATAGTTTATTTGAATTTTATTTTATTTTATTTTAAATTTTGGTAA 13032
QY 186 ATCAAAACAGTGTATTTCTTATACATGGTTCTTCAACTGGGAATAATGAAAACCTT 245
DB 13033 TTATTAATTTATATATGTTTATTAATTTGTTAATTTGTAAGAAATATTAATTAATGAAATT 13092
QY 246 CGTTGCTATGTGAAAGCTTTAATAGAAAAAGATGATTTTCTTGTAATTTGCGTCACTG 305

DB 13093 ATATAGTATATGTAATTAGAGTTTTTTACAGAAATAGAAAGTAATATATGCTGTATATAT 13152

QY 306 GAAGAAGGTCCTTGTAATGCTTTTCTTCAACAAAGGATGCTTTGGGTTATTCCAAAGC 365
DB 13153 GGAGAGATTTATTTTAAAGGAATGTTGATATAGTTATGAGAGGTTTGGTGAATTAATATT 13212

QY 366 CGTTGAAACACACGTCACGTTGGAAA-----ATTGTAGCTGATTTTACAAAAC 415
DB 13213 TGATGGAGAAAGTTCGTAGGTTGGAGATTTAAGAAAGATTTGTAATTTGAAGTTAAGGTA 13272

QY 416 TACTGTAGAAAAATATAAGTCTGATATCAAAATATACGATTGATCGG 464
DB 13273 GTTTGTTGAAAAATTAGGAAGAGTAGATGTTGATATTAAGTTTAGAGG 13321

RESULT 8

US-09-790-988-2
; Sequence 2, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7786
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-2

Query Match 4.4%; Score 45.8; DB 9; Length 7786;
Best Local Similarity 51.4%; Pred. No. 5.6;
Matches 133; Conservative 0; Mismatches 122; Indels 4; Gaps 1;

QY 70 TGTACTTTTAATGAGAAAGATATAGTATCTATGTTTACTCAAGGATAAGCGAGATGCT 129
DB 1229 TTTTATATATTTTCAAAATATATAAAATTTTATTTTATCTTTTCAATAATTAATTTT 1288
QY 130 ATTATCTTAAGAAAGAACTTTAAGCAATTACGATCTGTTTACAAAGTCTACAATATCA 189
DB 1289 TTATATTAAAGATATATACTTTTACTTTTATTTTATGAATTAATATATTTTATTA 1348
QY 190 AAACAAGTTGTAATTTCTTATACA---TGGTTTCTTCACTGGGAATATGAAAACCTT 245
DB 1349 AAAATATAATATTTTAAACATACATTTGATTATTTTCAAGATAACTTACTAAACTT 1408
QY 246 CGTTGCTATGTGAAAGCTTTAATAGAAAAAGATGATTTTCTTGTAATTTGCGTCACTG 305
DB 1409 AAAAGTTTATCTTAACCTTCTTAATTAATAATAATAATTAATTAATTAATTAATTAAT 1468
QY 306 GAAGAAGGTCCTTGTAAAT 324
DB 1469 CAAAAACAATATTTTAT 1487

RESULT 9

US-09-917-800A-1549
; Sequence 1549, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur

	Matches	159;	Conservative	0;	Mismatches	148;	Indels	15;	Gaps	1;
OY	318	TTGTAATGCTTTTGCTTCAACAAGGATGCTTGGGTTATTCCAAAGCCGTTGGAACAC	377							
Db	351	TTGCATTAAATTAGATTGGATCAACGGTTCACGGGAATACATCCATGCTGTAAACAATCT	410							
OY	378	ACGTCACGTTGGAAAATTGTAGCTGATTTTACAAAACCTACTTGTAGAAAAATATAAAGT	437							
Db	411	CCGTGTTGTTGGTGCTGAGGTGGCTTAATTTATTGATGTTCTCATGAAAAAATTTGAATA	470							
OY	438	GCTGATATCAAAATATACGATTGATCGGGCATAGTTGGGCGCGCATACTTCAGGTTTTC	497							
Db	471	TTCCCTTCTAAAGTGACCTTGATTGGCCACAGCTTGGAGCACACCTGGCTGGGGAAGC	530							
OY	498	GGGAAAAAGAAAGTTCAAAAGTTAAAAATTAGGAAAAATACAAGGAAATTATCGGGCTTGATCC	557							
Db	531	TGG-----GTCAAGGATATACCAGGCTTTGGAAGAAATACTGGGTTGAGACC	575							
OY	558	TGCTGGACCCGTAATTTTCATCGGAGTGACTGTCGGACAGACTTTGCGTAACAGACGACAGA	617							
Db	576	AGCTGGGCCAATTTTTCACAACACTCCAAGGAAGTCAGGCTAGACCCCTCGATGCCAA	635							
OY	618	ATATGTTCAAGTTATACATACA	639							
Db	636	CTTGTGACGTTATTCATACA	657							

RESULT 12
US-10-038

```

; Sequence 1, Application US/10038517
; Publication No. US20020115844A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. US20020115844A1 Human Lipase and Polynucleotides Encoding
; FILE REFERENCE: LEX-0293-USA
; CURRENT APPLICATION NUMBER: US/10/038,517
; PENDING FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 60/259,830
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-038-517-1

```

Query Match	4.3%;	Score 45.2;	DB 13;	Length 1404;
Best Local Similarity	49.4%;	Pred. No. 3.5;		
Matches 159;	Conservative	0;	Mismatches 148;	Indels 15;
				Gaps 1;

[illegible]

Db 636 CTTGTTGACGTTATTCATACA 657

RESULT 13
US-10-403-745-1

```

: Sequence 1, Application US/10403745
: Publication No. US20030165975A1
: GENERAL INFORMATION:
: APPLICANT: Khodadoust, Mehran
: APPLICANT: Kapeller-Libermann, Rosana
: TITLE OF INVENTION: No. US20030165975A1el Human Lipase Proteins, Nucleic Acides Encod
: TITLE OF INVENTION: Them, and Uses of Both of These
: FILE REFERENCE: 10147-14
: CURRENT APPLICATION NUMBER: US/10/403,745
: CURRENT FILING DATE: 2003-03-31
: PRIOR APPLICATION NUMBER: US/09/411,132A
: PRIOR FILING DATE: 2000-09-12
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 2352
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (2159)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (2307)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (2313)
: US-10-403-745-1

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Query Match	4.3%	Score 45.2;	DB 16;	Length 2352;
Best Local Similarity	49.4%	Pred. No. 4.5;		
Matches 159; Conservative	0;	Mismatches 148;	Indels 15;	Gaps 1;

[illegible]

RESULT 14

```

US-09-954-456-2217
; Sequence 2217, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76

```

```
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIORITY FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2217
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-2217
```

```
Query Match 4.3%; Score 45.2; DB 9; Length 3549;
Best Local Similarity 50.7%; Pred. No. 5.4;
Matches 144; Conservative 0; Mismatches 128; Indels 12; Gaps 1;
```

```
QY 365 CCGTTGAAACACACGTCACGTTGAAATTTGTAGCTGATTTACAAACTACTTGTAG 424
Db 545 CCGCGGCTACACCAACTGTGGGACAGATGTGCCCGTTTATCAACTGATGAGG 604
QY 425 AAAAATATAAGTGTGATATCAATATACGATTGATCGGGCATAGTTGGCGGCATA 484
Db 605 AGGAGTTTAACCTACCTCTGACCAATGTCATCTTGGGATACAGCCTTGAGCCCATG 664
QY 485 CTCAGGTTTTCGGGAAAGAGTCAAAAGTTAAATTTAGAAATACAGAAATTA 544
Db 665 CTGCTGGCATTCAGGAAGTCTGACCAATAAG-----AAAGTCAACAGAAATTA 712
QY 545 TCGGGCTTGATCTCTGTCGACCGTATTTTCATCGGAGTGAAGTCCGGACAGACTTTGCG 604
Db 713 CTGGCCTGATTCAGCTGACCTTAATTGAGTATGACAGAGCCCGAGTCGCTTTCTC 772
QY 605 TAACAGACGAGATATGTTCAAGTTATACATACATCAATCATTA 648
Db 773 CTGATGATGAGATTTTGTAGAGCTCTTACACACATTCACACAGA 816
```

RESULT 15

```
US-09-802-640-13
; Sequence 13, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsal Aruna
; APPLICANT: Kleya Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 13
; LENGTH: 3549
; TYPE: DNA
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; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (175)...(1602)
; OTHER INFORMATION: Nucleotide sequence encoding lipoprotein lipase
; OTHER INFORMATION: (LPL)
US-09-802-640-13
```

```
Query Match 4.3%; Score 45.2; DB 10; Length 3549;
Best Local Similarity 50.7%; Pred. No. 5.4;
Matches 144; Conservative 0; Mismatches 128; Indels 12; Gaps 1;
```

```
QY 365 CCGTTGAAACACACGTCACGTTGAAATTTGTAGCTGATTTACAAACTACTTGTAG 424
Db 545 CCGCGGCTACACCAACTGTGGGACAGATGTGCCCGTTTATCAACTGATGAGG 604
QY 425 AAAAATATAAGTGTGATATCAATATACGATTGATCGGGCATAGTTGGCGGCATA 484
Db 605 AGGAGTTTAACCTACCTCTGACCAATGTCATCTTGGGATACAGCCTTGAGCCCATG 664
QY 485 CTCAGGTTTTCGGGAAAGAGTCAAAAGTTAAATTTAGAAATACAGAAATTA 544
Db 665 CTGCTGGCATTCAGGAAGTCTGACCAATAAG-----AAAGTCAACAGAAATTA 712
QY 545 TCGGGCTTGATCTCTGTCGACCGTATTTTCATCGGAGTGAAGTCCGGACAGACTTTGCG 604
Db 713 CTGGCCTGATTCAGCTGACCTTAATTGAGTATGACAGAGCCCGAGTCGCTTTCTC 772
QY 605 TAACAGACGAGATATGTTCAAGTTATACATACATCAATCATTA 648
Db 773 CTGATGATGAGATTTTGTAGAGCTCTTACACACATTCACACAGA 816
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Search completed: April 29, 2005, 00:35:08
Job time : 743 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2005, 17:13:59 ; Search time 4076 Seconds
(without alignments)
9786.888 Million cell updates/sec

Title: US-10-688-011-1

Perfect score: 1048

Sequence: 1 attcgcttctgttagatga.....agtcataataaaaaaaaa 1048

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	61.4	5.9	883	7	CF378395	CF378395 AGENCOURT
2	60.2	5.7	343	1	AU261286	AU261286 AU261286
3	60.2	5.7	849	7	CF590524	CF590524 AGENCOURT
4	58.2	5.6	618	7	CK149622	CK149622 Camgest00
5	57.8	5.5	517	5	BU092097	BU092097 Mg_AFT_01
6	56.2	5.4	679	5	BM475141	BM475141 BM475141
7	54.6	5.2	715	5	BM332131	BM332131 BM332131
8	53.6	5.1	728	5	BM367531	BM367531 BM367531
9	52.8	5.0	1086	9	CNS00YXK	AL096962 Drosophila
10	52.4	5.0	665	7	CNS983321	CNS983321 51953_126
11	52	5.0	363	6	CA995600	CA995600 rg31f10.Y
12	51.8	4.9	1101	9	CNS00DT7	AL075293 Drosophila
13	51.4	4.9	708	5	BM365600	BM365600 BM365600
14	51.4	4.9	722	5	BM383883	BM383883 BM383883
15	51.4	4.9	758	5	BM420034	BM420034 BM420034
16	51.4	4.9	774	5	BM500776	BM500776 BM500776
17	51.4	4.9	883	5	BM482507	BM482507 BM482507
18	51.4	4.9	1101	9	CNS0039G	AL063921 Drosophila
19	50.4	4.8	435	6	CD738960	CD738960 4026720.1
20	49.6	4.7	1051	1	AA142285	AA142285 CK01198.C
21	49.6	4.7	1201	9	CNS0167M	AL106396 Drosophila
22	49.2	4.7	866	7	CO436102	CO436102 74592.127
23	48	4.6	770	7	CK352674	CK352674 AGENCOURT
24	48	4.6	1007	9	CNS00JOV	AL076752 Drosophila

C	25	47.8	4.6	238	9	CNS04CWO	AL285009 Tetraodon
	26	47.6	4.5	356	7	CO722219	CO722219 Mdftr3019i
	27	47.4	4.5	558	1	AV382351	AV382351 AV382351
C	28	47.4	4.5	615	7	CK134977	CK134977 RH13166.3
	29	47.4	4.5	653	6	CD647348	CD647348 AUF_107.L
	30	47.4	4.5	963	9	CNS00A4L	AL054918 Drosophila
	31	47.2	4.5	357	9	CNS028DK	AL185825 Tetraodon
	32	47.2	4.5	426	7	CO194538	CO194538 EC38727.5
C	33	47.2	4.5	1101	9	CNS016L1	AL106896 Drosophila
	34	47	4.5	237	7	CO185018	CO185018 EC29140.5
C	35	47	4.5	445	7	CF316695	CF316695 HD--06-B1
	36	47	4.5	599	6	CA964286	CA964286 CCLX04a14
	37	46.8	4.5	307	7	CK400031	CK400031 AGENCOURT
	38	46.8	4.5	1362	9	AG389060	AG389060 Mus muscu
	39	46.6	4.4	215	5	BM883483	BM883483 rc07d03.Y
	40	46.4	4.4	717	7	CN063847	CN063847 Ag2_p44_F
	41	46.4	4.4	1101	9	CNS000D1	AL065414 Drosophila
	42	46.2	4.4	890	9	CNS00AFU	AL055222 Drosophila
C	43	46	4.4	458	2	BF710972	BF710972 MI-P-AY1-
	44	45.8	4.4	581	5	BP257829	BP257829 BP257829
	45	45.8	4.4	766	6	CB998818	CB998818 AGENCOURT

ALIGNMENTS

RESULT 1
CF378395
LOCUS
DEFINITION
AGENCOURT_15349536 NICHG_XGC_Swb1n Xenopus tropicalis cDNA clone
IMAGE:7004912 5', mRNA sequence.
CF378395
CF378395.1 GI:34315839

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF378395 883 bp mRNA linear EST 27-AUG-2003
AGENCOURT_15349536 NICHG_XGC_Swb1n Xenopus tropicalis cDNA clone
IMAGE:7004912 5', mRNA sequence.
CF378395
CF378395.1 GI:34315839
EST.
Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Rob Granger, University of Virginia
cDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M14703 row: a column: 06
High quality sequence stop: 526.
Location/Qualifiers

FEATURES
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1..883
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7004912"
/tissue_type="whole body"
/clone_lib="NICHG_XGC_Swb1n"
/note="Vector: pEXpress-1; Site_1: EcoRV; Site_2: NotI;
Bulk tissue was collected from a whole 10 month old male
from the F6 strain. 1st strand cDNA was primed with a Not
I - oligo(dT) primer, double-stranded cDNA was cloned into
the Not I and EcoRV sites of pEXpress-1. Library was
size-selected for >1.5 kb fragments for an average insert
size of 1.92 kb. Library was normalized to Cot5 with a
180-fold reduction of actin. A non-normalized version of


```
PCR Primers
FORWARD: M13F
BACKWARD: pDNR11b_M13R
Plate: 01      row: A      column: 04
Seq primer: M13F
High quality sequence stop: 362..
Location/Qualifiers
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1. .517
/organism="Mesobuthus gibbosus"
/mol_type="mRNA"
/strain="Parga"
/db_xref="taxon:123226"
/clone="Mg_AFT_01A04"
/sex="female"
/tissue_type="Metasoma + Telson"
/dev_stage="adult"
/clone_lib="Mesobuthus gibbosus adult female tail"
/note="The Mesobuthus gibbosus EST library was prepared by Benjamin Gantenbein and Marian Thomson, University of Edinburgh. cDNA from the metasoma and telson of an adult female was cloned into the vector pDNR-LIB. ESTs were amplified from each clone by PCR, using primers pDNR.M13F and pDNR.M13R. The products were cleaned of excess nucleotides and phosphates, by treatment with SAP/ExoI, and then sequenced using pDNR.seq primer."

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ORIGIN

Query Match	5.5%	Score 57.8;	DB 5;	Length 517;
Best Local Similarity	53.1%;	Pred. No. 0.013;		
Matches 147; Conservative	0;	Mismatches 127;	Indels 3;	Gaps 1;

QY	397	GTAGCTGATTTTACAAAAC	CTCTGTAGAAAAATATAAAGTCTGATATCAAAATATACGA	456
Db	3	GTAGCATTTCTTCTCAAAAGTTTGA	CAGATCAATGCCGACTGCAAAACAATGAACGTTAAT	62
QY	457	TTGATCGGGCATAGTTTGGCGCGCA	TACTTCAGGTTTTGGGAAAAAGTAGTTCAAAAG	516
Db	63	GTCAATGGGCATAGTTTAGGATCTCA	TATTTGCATCTTACGCTGGATCAGGTATTAAGAA	122
QY	517	TTAAATTAGGAAAATACAGA	AAATTAATCGGCTTGATCTGCTGACCGTATTTTCAT	576
Db	123	TATAATTTGACTTTAGGAAG--	-AATACTGGATTGGATCTGCTGCAACCTTATTTTCAA	179
QY	577	CGGAGTGACTGTCCGGACAGACTT	TCGCTAACAGACCGCAGAAATATGTTCAAGTTATACAT	636
Db	180	AATATGCCACAAATAGTGAGATT	AGATCCATCAGATGCCCAATTTGTTGATGCTATACAT	239
QY	637	ACATCAATCATATTAGGAGTA	TATTAATGTTGGTA	673
Db	240	ACAGATGAAAAATCTATACT	ACTTTTAGGTTTGGAA	276

RESULT 6
 BW475141
 LOCUS
 DEFINITION
 BW475141 679 bp mRNA linear EST 11-JUN-2004
 BW475141 Nori Satoh unpublished cDNA library, mature adult whole
 animal Ciona intestinalis cDNA clone c1ma012m23 5', mRNA sequence.
 BW475141
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Ciona intestinalis
 Ciona intestinalis
 Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 Phlebobranchia; Clonidae; Ciona.
 1 (bases 1 to 679)
 Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
 Expressed genes in Ciona intestinalis (2004)
 Unpublished (2004)
 COMMENT
 Contact: Nori Satoh

Department of Zoology
Kyoto University
Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081

FEATURES
source 1. .679

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/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cima012m23"
/tissue_type="whole animal"
/dev_stage="mature adult"
/clone_lib="Nori Satcho unpublished cDNA library, mature
adult whole animal"

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ORIGIN

Query Match	5.4%	Score 56.2;	DB 5;	Length 679;
Best Local Similarity	53.9%	Pred. No. 0.031;		
Matches 159; Conservative	0;	Mismatches 133;	Indels 3;	Gaps 2;

QY 348 TTTGGGTTATTCCAAAGCCGTTGGAAACACACGTCACGTTGGAAAAATTGTAGCTGATTT 407

Db 352 TGTTGAATAACGACAACGCTGCTTCAAAACACGCGTCTGTAGAGACACAAGTTGGTTTTCT 411

QY 408 TACAAAACCTACTTGTAGAAAAATATAAAGTCTGATATCAATATATACGATTGATCGGGCA 467

Db 412 TATCAAAATGTTAATGAGGTGCGTAAACGCTCGCGCTGAAAACTTCACCTTGTGCGCTT 471

QY 468 TAGTTTGGGCGCGCATACTTCAGGTTTTCGGGAAAAAGAGTTCA-AAAGTTAAAAATTAG 526

Db 472 CAGTTTGGGTCACATGTAGACAGGGTTTGCCGGTAAAAACGTCACAGCAAGCCGGGAAGAG 531

QY 527 GAAAAATCAAGGA--AATTATCGGGCTTGATCCTGCTGGAACCGTATTTTCATCGGAGTGA 584

Db 532 GCACACCCGTTGGACGAATTAACCGGTTTAGATCCGGCCAACCCGGGATTCAAATTCTGCACAA 591

QY 585 CTGTCGGGACAGACTTTGCGGTAACAGACGCAGAAATATGTTCAAGTTATATACATACA 639

Db 592 CTGCTCCGTCAGACTCGACCGGTTCTGACGCAAAATTCGTAGATGTTATTCACACA 646

RESULT	7
BW332131	
LOCUS	715 bp mRNA linear EST 27-MAY-2004
DEFINITION	BW332131 Yutaka Satou unpublished cDNA library, adult digestive gland Ciona intestinalis cDNA clone cidg841f12 5', mRNA sequence.
ACCESSION	BW332131
VERSION	BW332131.1 GI:47743932
KEYWORDS	EST.
SOURCE	Ciona intestinalis
ORGANISM	Ciona intestinalis

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 715)	Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.	Expressed genes in <i>Ciona intestinalis</i> (2004)	Unpublished (2004)	Contact: Yutaka Satou

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp

FEATURES	Location/Qualifiers
source	1. .715

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/organisms="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cldg841f12"
/tissue_type="digestive gland"
/dev stage="adult"
/clone_lib="Yutaka Satou unpublished cDNA library, adult
digestive gland"

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ORIGIN

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Query Match      5.2%; Score 54.6; DB 5; Length 715;
Best Local Similarity 53.0%; Pred. No. 0.073;
Matches 151; Conservative 0; Mismatches 119; Indels 15; Gaps 1;

QY 354 TTATTCCAAAGCCGTTGGAACACACGTCACGTTGGAAAAATTGTAGCTGATTTTACAAA 413
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 426 TTACGCCCAAGCTACCGCAACACTGCTGTCGTAGGGCGGAGATTGCTCTTTAATTAA 485

QY 414 ACTACTGTAGAAAAATATAAGTCTGATATCAAAATATACGATTGATCGGCAATAGTTT 473
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 486 CAGGCTTGAGGAGCAATCAGAGCTTTGGAAGAAGATGCTCACATATTCGGGACAGCTT 545

QY 474 GGGCGGCATACTTCAGGTTTTCGGGAAAAAGAGTTCAAAAAGTTAAATTAGGAAAAATA 533
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 546 GGGCGCACACGTTGCTGCTATGCTGTGTAAGATTAAACGTTTAGTGC----- 596

QY 534 CAAGGAATTAATCGGGCTGATCCTGCTGACCGGTATTTTCATCGAGTGACTGTCGGA 593
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 597 -----AATTACGGGCTGGATCCAGCTGAGCCGTTTATCAAGGAACGATCCGTAAGT 650

QY 594 CAGACTTTGCGTTAACAGACGACAGATATGTTCAAGTTATACATAC 638
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 651 ACGGCTCGACCCACAGACGCGCTGTATGTGATGCCATACATAC 695

RESULT 8
LOCUS      BM367531      728 bp      mRNA      linear      EST 28-MAY-2004
DEFINITION BM367531 Yutaka Satou unpublished cDNA library, mature adult whole
            animal Ciona intestinalis cDNA clone cima841k24 5', mRNA sequence.
ACCESSION  BM367531
VERSION     BM367531.1  GI:47783359
KEYWORDS   EST.
SOURCE      Ciona intestinalis
ORGANISM   Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Clonidae; Ciona.
REFERENCE   1 (bases 1 to 728)
AUTHORS    Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
TITLE      Expressed genes in Ciona intestinalis (2004)
JOURNAL    Unpublished (2004)
COMMENT    Contact: Yutaka Satou
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto 606-8502, Japan
            Tel: 81-75-753-4095
            Fax: 81-75-705-1113
            Email: yutaka@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source     1..728
            /organism="Ciona intestinalis"
            /mol_type="mRNA"
            /db_xref="taxon:7719"
            /clone="cima841k24"
            /tissue_type="whole animal"
            /dev_stage="mature adult"
            /clone_lib="Yutaka Satou unpublished cDNA library, mature
            adult whole animal"

ORIGIN
Query Match      5.1%; Score 53.6; DB 5; Length 728;
Best Local Similarity 52.6%; Pred. No. 0.12;
Matches 150; Conservative 0; Mismatches 120; Indels 15; Gaps 1;

QY 354 TTATTCCAAAGCCGTTGGAACACACGTCACGTTGGAAAAATTGTAGCTGATTTTACAAA 413
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 433 TTACGCCCAAGCTACCGCAACACTGCTGTCGTAGGGCGGAGATTGCTCTTTAATTAA 492

QY 414 ACTACTGTAGAAAAATATAAGTCTGATATCAAAATATACGATTGATCGGCAATAGTTT 473
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 493 CAGGCTTGAGGAGCAATCAGAGCTTTGGAAGAAGATGCTCACATTTATCGGGACAGCTT 552

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QY 474 GGGCGGCATACTTCAGGTTTTCGGGAAAAAGAGTTCAAAAGTTAAAAATTAGGAAAAATA 533
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 553 GGGCGCACACGTTGCTGCTATGCTGTGTAAGATTAAACGTTTAGTGC----- 603

QY 534 CAAGGAATTAATCGGGCTGATCCTGCTGACCCGTATTTTCATCGAGTGACTGTCGGA 593
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 604 -----AATTACGGGCTGGATCCAGCTGAGCCGTTTATCAAGGAACGATCCCGTAGT 657

QY 594 CAGACTTTGCGTTAACAGACGACAGATATGTTCAAGTTATACATAC 638
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 658 ACGGCTCGACCCNACAGACGCGCTGTATGTGATGCCATACATAC 702

RESULT 9
LOCUS      CNS00YXK      1086 bp      DNA      linear      GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN01M03 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION  AL096962
VERSION     AL096962.1  GI:5608573
KEYWORDS   GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1086)
AUTHORS    Genoscope.
TITLE      Direct Submission
JOURNAL    Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT    Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPIH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBelOBAC11.

FEATURES
source     1..1086
            /organism="Drosophila melanogaster"
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            /note="end : T7"

ORIGIN
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Best Local Similarity 30.9%; Pred. No. 0.2;
Matches 63; Conservative 61; Mismatches 80; Indels 0; Gaps 0;

QY 844 AGAGAGACACCTGTGTTGGCTTGATGAATGCAAAAAGTTATCTGCTAGAGCGCA 903
    ||:| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 775 AGRKANNNGRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 834

QY 904 TTTATGACCGGTTGAAGCAATGCACCTTATTGCCATTAACGAGGGATTAACTTTAA 963
    :||:| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 835 AAWTWGKAAATTKTNAKTTRAAAAATTWAAAAWWMTKTWTWTWTAWWAAAAATTWT 894

QY 964 TTATAACAAGAGTCAATGTACACAAAAATGTATCTATGTGATGAATATTAAATGAATAA 1023
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 895 TTATAWMAAAWAGTTWAAAAAAWTATAAAWATTATTTTWTAAAWAWATWAWTTAAWMA 954

QY 1024 CGAACAGTCAAAATAAAAAAAA 1047
    :| : : : : : : : : : : : : : : : : : : : : : : : : :
DB 955 AAWAWATAATTWTAATAATKAWMAA 978

```


RESULT 10	
CN983321	LOCUS
DEFINITION	CN983321 665 bp mRNA linear EST 08-JUN-2004
ACCESSION	51953_126_038_D04 Fundulus heteroclitus Liver Fundulus heteroclitus
VERSION	cDNA similar to Triacylglycerol lipase, hepatic precursor (EC 3.1,
KEYWORDS	mRNA sequence.
SOURCE	CN983321 GI:48464912
ORGANISM	Fundulus heteroclitus (killifish)
	Fundulus heteroclitus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
	Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomomorpha;
	Cyprinodontiformes; Fundulidae; Fundulus.
REFERENCE	1 (bases 1 to 665)
AUTHORS	Crawford,D.L., Oleksiak,M.F., Kolell,K.J., Paschall,J., VanWye,J.,
	Roach,J.L. and Whitehead,J.A.
TITLE	Fundulus Functional Genomics: EST Database for Teleost Fish
JOURNAL	Unpublished (2004)
COMMENT	Contact: Crawford, Douglas L. Marine Genomics - Crawford Lab Rosenstiel School of Marine and Atmospheric Science - University of Miami 4600 Rickenbacker Causeway, Miami, FL 33149-1098 USA Tel: 305 361 4121 Email: dcrawford@rsmas.miami.edu Database Web Interface http://genomics.rsmas.miami.edu/funnybase/super_craw3/ Plate: 38 row: D column: 4.
FEATURES	Location/Qualifiers
source	1..665
	/organism="Fundulus heteroclitus"
	/mol_type="mRNA"
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	/tissue_type="Liver"
	/clone_lib="Fundulus Heteroclitus Liver"
	/note="Organ: Liver"
ORIGIN	
Query Match	5.0%; Score 52.4; DB 7; Length 665;
Best Local Similarity	51.4%; Pred. No. 0.23;
Matches 150; Conservative	0; Mismatches 136; Indels 6; Gaps 1;
OY	354 TTATTCCAAAGCCGTTGGAACAACACGTCACGTTGGAATAATTTGTAGCTGATTTTACA 413
Db	
	367 TTATCCCCCTGGCTGTGCAGACACC CGCACTGTGGCGAAGATATAGCTCATCTGCTGCA 426
OY	414 ACTACTTGTAAGAAAATATAAAGTGCTGATATCAAATATAAGATTGATCGGGCATACTT 473
Db	
	427 GTCTCTTCAGAGAAGATACCGGTAACCCGGTAGAAGAAAGCTCATCTGATTGGATACAGCCT 486
OY	474 GGGCGCGCATCTTCAGGTTTTGCGGGAAAAAGAGTTCAAAAAGTTAAATTAGAAAAATA 533
Db	
	487 GGGAGCGCACATATCTGGGTTTGCTGGAAGCTTCTGCAAGGTTCAAGC-----AAGAT 540
OY	534 CAAGGAATATATCGGGCTTGATCTGCTGACCGGTAATTTTCATCGAGTGACTGTCCGA 593
Db	
	541 CCGGAGGATTACCGCGCTGATCCGGCAGGCGCGCTGTTGAGGGCATGTCTCCACGGA 600
OY	594 CAGACTTTGCGTAACAGACGAGATATGTTCAAGTTATACATACATCAATC 645
Db	
	601 CCGACTTTCTCCGATGACGACAGAGTTTGTGACGCCATCCACACCTTCACC 652
RESULT 11	
LOCUS	CA995600 363 bp mRNA linear EST 07-JAN-2003
DEFINITION	rg3lf10.y1 Meloidogyne hapla U2 SL1 TOPO v1 Meloidogyne hapla cDNA
ACCESSION	CA995600
VERSION	CA995600.1 GI:27540471
KEYWORDS	EST.

[illegible]

SOURCE ORGANISM	TITLE JOURNAL	REFERENCE AUTHORS
Drosophila melanogaster (fruit fly)		
Drosophila melanogaster		
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
1 (bases 1 to 1101)		
Genoscope.		
Direct Submission		
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :		
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr		
- Web : www.genoscope.cns.fr)		
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).		
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.		
location/Qualifiers		
1..1101		
/organism="Drosophila melanogaster"		
/mol_type="genomic DNA"		
/db_xref="taxon:7227"		
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/clone_1b="RPCI-98"		
/note="end : TET3"		
ORIGIN		
Query Match	4.9%; Score 51.8; DB 9; Length 1101;	
Best Local Similarity	30.8%; Pred. No. 0.33;	
Matches 125; Conservative 73; Mismatches 208; Indels 0; Gaps 0;		
OY	33 TAGAATGTGACTTGATAGAGGCATGCTCCGGATTGTACTTTAATGAGAAGATAT	92
DB	1101 TAAAWATAWTTTAAWTATTAWTWTWTATTTAAAWATAWATAATAATATTTAT	1042
OY	93 AGTATTCATGTTACTCAAGGATAAGCAGATGTAATATCTTAGAAGAACAATT	152
DB	1041 TTATATTATATATWTTATATATATWTTTWTATAMATWTAATTTTWTWTWWATTTWT	982
OY	153 AACGAATTACGATCGTTTACCAAAGCTACAATATCAAAACAAGTTGTAATCTTATACA	212
DB	981 WWWWTTTTTTTWTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	922
OY	213 TGGTTCCCTTCACTGGGAATATGAAAACCTTCGTTCTATGCGAAAGCTTTAATAGA	272
DB	921 TWTTTTWTATWATWTAATWTAATWTAATWTAATWTAATWTAATWTAATWTAATWTAATWTTT	862
OY	273 AAAAGATGATTTCTGTGAATTTCCGTCGACTGGAAGAGGCTGTGTAATGCTTTGC	332
DB	861 ATTWTTTWTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	802
OY	333 TTCACAAAGATGCTTTGGGTTATTCCAAAGCCGTTGGAACAACACAGTCACGTTGGA	392
DB	801 BSBBVBNNVNTTTTNNNNNNNNHRRRRRRRRRRGRGRGGRGNNNNNNNNRRA	742
OY	393 ATTTGATGATTTTACAAACTACTTGTAGAAAAATATAAAGTG	438
DB	741 AAAGAGGATGWTATAKRAAGTAAGAADRAARRARRRRARG	696
RESULT 13		
BW365600	708 bp mRNA linear EST 28-MAY-2004	
BW365600	Yutaka Satou unpublished cDNA library, mature adult whole	
DEFINITION	BW365600 Yutaka Satou unpublished cDNA library, mature adult whole	

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT		
animal Ciona intestinalis cDNA clone cima836c06 5', mRNA sequence.	BM365600	EST.	Ciona intestinalis	Ciona intestinalis	Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; phlebobranchia; Clonidae; Ciona.	Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.	Expressed genes in Ciona intestinalis (2004)	Unpublished (2004)	Contact: Yutaka Satou Department of Zoology Kyoto University Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-4095 Fax: 81-75-705-1113 Email: yutaka@ascidian.zool.kyoto-u.ac.jp.		
FEATURES	source	1..708	Location/Qualifiers	1..708	Location/Qualifiers	1..708	Location/Qualifiers	1..708	Location/Qualifiers		
Query Match	Best Local Similarity	4.9%;	Score 51.4;	DB 5;	Length 708;	Matches 149;	Conservative 0;	Mismatches 121;	Indels 15;	Gaps 1;	
354	TTATTCCAAAGCCGTTGGAACACACAGCTCACGTTGGAATAATTGTAGCTGATTTACAA	413									
429	TTACGGCCAAAGCTACCGCCCAACACTCGTGTGTTAGGGCGGAGATTGCTCTTAATTAA	488									
414	ACTACTTGTAAGAAATATAAAGTGCTGATATCAATAATACGATTGATCGGGCATAGTT	473									
489	CAGGCTTGAGGAGCAATCAGGAGCCTTGGAAGAAATGCTCATATCATCGGACACAGCTT	548									
474	GGGCGGCATACCTTCAGGTTTTCGCGGAAAGAAAGTTCAAAAAGTTAAATTAGAAATA	533									
549	GGGCGCACACGTTGCTGGCTATGCTGTGTAAGATTAAACGTTTAGTCTG-----	599									
534	CAAGGAATTATTCGGGCTTGATCTGCTGAGACCGTATTTTCATCGGAGTGACTGTCGGA	593									
600	-----AATTACCGGCTTGATCCAGCTGAGCCGTTTATCAAGAACGATCCCGTAGT	653									
594	CAGACTTTCGCTAACAGACGAGATATGTTCAAGTTATACATAC	638									
654	ACGGCTCGACCCACAGACGCGCTGATGTGATGCCATACATAC	698									
RESULT 14	BM383883/c	722 bp	mRNA	linear	EST 28-MAY-2004	BM383883	Yutaka Satou unpublished cDNA library, adult digestive	gland Ciona intestinalis cDNA clone cidg834k21 3', mRNA sequence.	BM383883	BM383883.1	GI:47799711
DEFINITION	BM383883	Yutaka Satou unpublished cDNA library, adult digestive	gland Ciona intestinalis cDNA clone cidg834k21 3', mRNA sequence.	BM383883	BM383883.1	GI:47799711	EST.	Ciona intestinalis	Ciona intestinalis	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; phlebobranchia; Clonidae; Ciona.	
REFERENCE	AUTHORS	Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.	Expressed genes in Ciona intestinalis (2004)	Unpublished (2004)	Contact: Yutaka Satou Department of Zoology Kyoto University Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-4095 Fax: 81-75-705-1113 Email: yutaka@ascidian.zool.kyoto-u.ac.jp.						
ORIGIN	Query Match	Best Local Similarity	4.9%;	Score 51.4;	DB 5;	Length 708;	Matches 149;	Conservative 0;	Mismatches 121;	Indels 15;	Gaps 1;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2005, 17:08:05 ; Search time 4887 Seconds
(without alignments)
10391.051 Million cell updates/sec

Title: US-10-688-011-1

Perfect score: 1048

Sequence: 1 atttgcttctgttagatga.....agtcataataaaaaaaaaa 1048

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1048	100.0	1048	3	AF174527	AF174527 Polistes
2	1048	100.0	1048	6	BD223803	BD223803 Cloning a
3	1048	100.0	1048	6	AR206946	AR206946 Sequence
4	1048	100.0	1048	6	AR431328	AR431328 Sequence
5	818.4	78.1	1171	3	AY566645	AY566645 Polistes
6	782.4	74.7	948	3	AY566646	AY566646 Polistes
7	779.2	74.4	948	3	AY566647	AY566647 Polistes
8	777.6	74.2	948	3	AY566649	AY566649 Polistes
9	441	42.1	1050	6	AR162936	AR162936 Sequence
10	441	42.1	1050	6	AR167265	AR167265 Sequence
11	441	42.1	1050	6	I33765	I33765 Sequence 16
12	441	42.1	1050	6	I36978	I36978 Sequence 16
13	441	42.1	1050	6	AR206926	AR206926 Sequence
14	429.4	41.0	1324	3	VESAPV1R	L43561 Vesputia vul
15	426.2	40.7	1341	6	AR162937	AR162937 Sequence
16	426.2	40.7	1341	6	AR167266	AR167266 Sequence
17	426.2	40.7	1341	6	I33766	I33766 Sequence 26
18	426.2	40.7	1341	6	I36979	I36979 Sequence 26
19	426.2	40.7	1341	6	AR206927	AR206927 Sequence

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22	59	5.6	1141	6	AX083744	AX083744 Sequence
23	51.2	4.9	3213	4	MVLIPOLIP	AJ223493 Mustela v
24	50.2	4.8	12353	1	AE007710	AE007710 Clostridi
25	49.8	4.8	1511	4	FC042725	U42725 Felis catus
26	49.2	4.7	14536	3	AF467260	AF467260 Ostrinia
27	49	4.7	1301	6	CQ578568	CQ578568 Sequence
28	49	4.7	1338	3	AY094909	AY094909 Drosophil
29	49	4.7	4016	6	CQ578567	CQ578567 Sequence
30	49	4.7	51050	3	AC004340	AC004340 Drosophil
31	49	4.7	85539	2	AC019877	AC019877 Drosophil
32	49	4.7	175867	3	AC007976	AC007976 Drosophil
33	49	4.7	184650	3	AC092186	AC092186 Drosophil
34	49	4.7	303641	3	AE003583	AE003583 Drosophil
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36	48.2	4.6	1384	3	AF489470	AF489470 Ceratobae
37	48.2	4.6	1733	5	BC053243	BC053243 Danio rer
38	48.2	4.6	105682	3	AC116957_3	Continuation (4 of
39	48	4.6	1595	4	AY559452	AY559452 Sus scrof
40	47.6	4.5	14535	3	AF442957	AF442957 Ostrinia
41	47.6	4.5	85467	9	AL133457	AL133457 Human DNA
42	47.6	4.5	146706	2	CR450735	CR450735 Danio rer
43	47.6	4.5	184610	2	AC009924	AC009924 Homo sapi
44	47.4	4.5	12184	3	AY372120	AY372120 Plasmodiu
45	47.4	4.5	250029	3	AE014839	AE014839 Plasmodiu

ALIGNMENTS

RESULT 1
AF174527 1048 bp mRNA linear INV 01-SEP-1999
LOCUS Polistes annularis phospholipase A1 mRNA, complete cds.
DEFINITION Polistes annularis phospholipase A1 mRNA, complete cds.
ACCESSION AF174527
VERSION AF174527.1 GI:5815248
KEYWORDS
SOURCE Polistes annularis
ORGANISM Polistes annularis
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Polistinae; Polistes.
REFERENCE 1 (bases 1 to 1048)
AUTHORS King, T.P. and Lu, G.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Rockefeller University, 1230 York Ave., New York, NY 10021, USA
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source location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1048; DB 3; Length 1048;
Best Local Similarity 100.0%; Pred. No. 9, 1e-195;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATTTCGCTTCTGTAGATGATTCGACGACATTTAGAAATGTGATCCTTGAAATGAGGCATG 60
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Db	1	ATTGCTCTCTGTTAGATGATTCGACGACATTGAAATGCTTGAATAGAGGCATG	60
Qy	61	TCTCCGGATTGTAATTTAATGAGAAAGATATAGTATTTCTATGTTTACTCAAGGATAG	120
Db	61	TCTCCGGATTGTAATTTAATGAGAAAGATATAGTATTTCTATGTTTACTCAAGGATAG	120
Qy	121	CGAGATGATATTATTTCTTAAGAAAGAACTTTAAGAAATTAGATCTGTTTACAAGTCT	180
Db	121	CGAGATGATATTATTTCTTAAGAAAGAACTTTAAGAAATTAGATCTGTTTACAAGTCT	180
Qy	181	ACAATATCAAAACAAGTTGATTTCTTATACATGTTTCTTCAACTGGGAATAATGAA	240
Db	181	ACAATATCAAAACAAGTTGATTTCTTATACATGTTTCTTCAACTGGGAATAATGAA	240
Qy	241	AACTTCGTGCTATGTCGAAAGCTTTAATAGAAAAGATGATTTTCTGTAATTCGGTC	300
Db	241	AACTTCGTGCTATGTCGAAAGCTTTAATAGAAAAGATGATTTTCTGTAATTCGGTC	300
Qy	301	GACTGGAAGAGGGTCTGTAATGCTTTTGCTTCAACAAGAGTCTTGCGTTATTC	360
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Qy	361	AAAGCCGTGGAACAACGTCACGTTGAAAAATTGTAGCTGATTTTACAACAACTACTT	420
Db	361	AAAGCCGTGGAACAACGTCACGTTGAAAAATTGTAGCTGATTTTACAACAACTACTT	420
Qy	421	GTAGAAAAATATTAAGTCTGATATCAAAATATACGATGATCGGCACTGTTGGCGCG	480
Db	421	GTAGAAAAATATTAAGTCTGATATCAAAATATACGATGATCGGCACTGTTGGCGCG	480
Qy	481	CATACTTCAGGTTTTCGGGAAAAAGAGTTCAAAAGTTAAATTAGAAAAATACAAGAA	540
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Qy	781	TGTTGTTTAATGGAACACCATGGAAGAATATTTACGACACTCCAAAACCAATTTCCAG	840
Db	781	TGTTGTTTAATGGAACACCATGGAAGAATATTTACGACACTCCAAAACCAATTTCCAG	840
Qy	841	TGCAGAGGAGACACCTGCTGTTGCGTTGATGATGCAAAAAAGTTATCTGCTAGAGGC	900
Db	841	TGCAGAGGAGACACCTGCTGTTGCGTTGATGATGCAAAAAAGTTATCTGCTAGAGGC	900
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Db	901	GCAATTTATGACCCGGTGAAGCAATGCACTTATTCATTAACGAGGGGATTAACCTT	960
Qy	961	TAAATATAAACAAGTCAATGTACACAAAAATGTATCTATGATGATAATTAATGAAT	1020
Db	961	TAAATATAAACAAGTCAATGTACACAAAAATGTATCTATGATGATAATTAATGAAT	1020
Qy	1021	AAACGAACAGTCAAAATAAAAA	1048
Db	1021	AAACGAACAGTCAAAATAAAAA	1048

RESULT 2
BD223803

LOCUS	BD223803	1048 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Cloning and recombinant production of polistinae toxin enzymes (phospholipase, hyaluronidase, etc.) and immunological therapy based thereon.				
ACCESSION	BD223803				
VERSION	BD223803.1	GI:33033573			
KEYWORDS	JP 2002525107-A/1.				
SOURCE	Polistes annularis				
ORGANISM	Polistes annularis				
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Polistinae; Polistes.				
AUTHORS	1 (bases 1 to 1048)				
TITLE	Cloning and recombinant production of polistinae toxin enzymes (phospholipase, hyaluronidase, etc.) and immunological therapy based thereon				
JOURNAL	Patent: JP 2002525107-A 1 13-AUG-2002;				
COMMENT	THE ROCKEFELLER UNIVERSITY				
	OS	Polistes annularis			
	PN	JP 2002525107-A/1			
	PD	13-AUG-2002			
	PF	01-OCT-1999 JP 2000572343			
	PR	01-OCT-1998 US 09/166205			
	PI	TE PAIO KING			
	PC	C12N15/09,A61K38/46,A61K48/00,A61P31/12,A61P31/18,A61P37/06,A61P37/08,			
	PC	C07K19/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/16,C12N9/26,C12N15/00,			
	PC	C12N5/00,A61K37/54			
	CC	Cloning and recombinant production of polistinae toxin enzymes			
	CC	(phospholipase, hyaluronidase, etc.) and immunological therapy based			
	CC	thereon			
	FH	Key			
	FT	source			
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Best Local Similarity	100.0%; Pred. No. 9.1e-195;				
Matches 1048; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	ATTGCTTCTTGTAGATGATTCGACGACATTGAAATGTAACCTTGAATAGAGCATG	60		
Db	1	ATTGCTTCTTGTAGATGATTCGACGACATTGAAATGTAACCTTGAATAGAGCATG	60		
Qy	61	TCTCCGATTGTACTTTTAATGAGAAAGATATAGTATTTCTATGTTTACTCAAGGATAG	120		
Db	61	TCTCCGATTGTACTTTTAATGAGAAAGATATAGTATTTCTATGTTTACTCAAGGATAG	120		
Qy	121	CGAGATGTAATTATTTCTTAAGAAAGAACTTTAAGCAATTACGATCTGTTTACAAGTCT	180		
Db	121	CGAGATGTAATTATTTCTTAAGAAAGAACTTTAAGCAATTACGATCTGTTTACAAGTCT	180		
Qy	181	ACAATATCAAAACAAGTTGTAATTTCTTATACATGTTTCTTCAACTGGGAATAATGAA	240		
Db	181	ACAATATCAAAACAAGTTGTAATTTCTTATACATGTTTCTTCAACTGGGAATAATGAA	240		
Qy	241	AACTTCGTGCTATGTCGAAAGCTTTAATAGAAAAGATGATTTCTTGAATTTCCGTC	300		
Db	241	AACTTCGTGCTATGTCGAAAGCTTTAATAGAAAAGATGATTTCTTGAATTTCCGTC	300		
Qy	301	GACTGGAAGAGGGTCTGTAATGCTTTTGCTTCAACAAGAGATGCTTTGGGTTATTC	360		
Db	301	GACTGGAAGAGGGTCTGTAATGCTTTTGCTTCAACAAGAGATGCTTTGGGTTATTC	360		

Qy 361 AAAGCCGTGGAAACACACGTCACGTTGGAAAAATTGTAGCTGATTTTACAAACTACTT 420
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Db 361 AAAGCCGTGGAAACACACGTCACGTTGGAAAAATTGTAGCTGATTTTACAAACTACTT 420
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Db 421 GTAGAAAAATATAAAGTGTGATATCAATATATACGATTGATCGGCGATAGTTGGCGCG 480
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Db 481 CATACTTCAGGTTTTCGCGGAAAAAGTTCAAAAGTTAAAAATTAGAAAAATACAGGAA 540
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Db 1021 AAACGAACAGTCAAAATAAAAAAA 1048

RESULT 3
AR206946 1048 bp DNA linear PAT 20-JUN-2002
LOCUS AR206946
DEFINITION Sequence 63 from patent US 6372471.
ACCESSION AR206946
VERSION AR206946.1 GI:21505701
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1048)
AUTHORS King,T.Piao.
TITLE Cloning and recombinant production of vespid venom enzymes, such as phospholipase and hyaluronidase, and immunological therapies based thereon
JOURNAL Patent: US 6372471-A 63 16-APR-2002;
FEATURES Location/Qualifiers
Source 1..1048
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Query Match 100.0%; Score 1048; DB 6; Length 1048;
Best Local Similarity 100.0%; Pred. No. 9.1e-195;

Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1021 AAACGAACAGTCAAAATAAAAAAA 1048

RESULT 4
AR431328 1048 bp DNA linear PAT 18-DEC-2003
LOCUS AR431328
DEFINITION Sequence 1 from patent US 6652851.
ACCESSION AR431328
VERSION AR431328.1 GI:40193344
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1048)
AUTHORS King,T.P.
TITLE Cloning and recombinant production of polistine venom enzymes, such as phospholipase and hyaluronidase, and immunological therapies based thereon
JOURNAL Patent: US 6652851-A 1 25-NOV-2003;
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Query Match 100.0%; Score 1048; DB 6; Length 1048;
Best Local Similarity 100.0%; Pred. No. 9.1e-195;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATTTGCTTCTGTTAGATGATTCGACGACATTTGAAGTGTACCTGAATAGAGCATG 60
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Db 481 CATACTTCAGGTTTTCGCGGAAAAAGAGTTCAAAAGTTAAATTTAGGAAAAATACAAGGAA 540
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QY 1021 AAACGACAGTCAAAATTAATAAAAAA 1048
Db 1021 AAACGACAGTCAAAATTAATAAAAAA 1048

RESULT 5
AY566645 1171 bp mRNA linear INV 22-MAR-2004
LOCUS AY566645
DEFINITION Polistes dominulus venom phospholipase A1 precursor mRNA,
complete cds.
ACCESSION AY566645
VERSION AY566645.1 GI:45510886
KEYWORDS
SOURCE Polistes dominulus (European paper wasp)
ORGANISM Polistes dominulus
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
Vespoidea; Vespidae; Polistinae; Polistes.
REFERENCE 1 (bases 1 to 1171)
Moawad,T.I.S. and Hoffman,D.R.
AUTHORS Direct Submission
TITLE Submitted (05-MAR-2004) Pathology and Laboratory Medicine
JOURNAL Department, Brody School of Medicine, East Carolina University, 600
Moye Blvd., Greenville, NC 27858, USA
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Best Local Similarity 86.9%; Pred. No. 6.4e-150;	
Matches 911; Conservative 0; Mismatches 136; Indels 1; Gaps 1;	
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Qy	61 TCTCCGATGTACTTTTAATGAGAAAGATAGTATTCTATGTTTACTCAAGGAGTAAG 120
Db	166 ACTCCGATGTACTTTTAATGAGAAAGATATAGAGCTACAGCTTACTCAAGGAGTAAA 225
Qy	121 CGAGATGGTATTATTCTTAAGAAAGAACTTTAACGAATTACGATCTGTTTACAAGTCT 180
Db	226 CGAATGGTATTATTCTTAAGAAAGAAATTTAAAGAATTACGATCTGTTCAAAAATCT 285
Qy	181 ACAATATCAAAACAAGTGTATTCTTATACATGGTTCCCTTCAACTGGGAATTAAGAA 240
Db	286 CAATATACATCAAAATGCAATTCTTATACATGGTTCCCTTCAACTGGGAATTAAGAA 345
Qy	241 AACTTCGTTGCTATGTCGAAAGCTTTAATAGAAAAAGATGATTTCTGTAATTCGGTC 300
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Qy	301 GACTGGAAGAAGGCTGTGTAATGCTTTGCTTCAACAAAGAGATGCTTTGGGTTATCC 360
Db	406 GACTGGAAGAAGGCTGTGCAATGCTTTGCTTCAACTAATGATGTTTGGGTTACTCC 465
Qy	361 AAAGCCGTTGGAACAACACGTCACGTTGGAATAATTTGAGCTGATTTTACAAAATACTT 420
Db	466 CAAGCCGTTGGAACAACACGTCACGTTGGAATAATGAGCTGATTTTACAAAATTATTA 525
Qy	421 GTAGAAAATAATAAGTCTGATATCAAAATATACGATTGATCGGGCATAGTTGGGCGG 480
Db	526 GTAGAACATAATAAGTCCGATGTCGAATATACGATTGATCGGCCATAGTTGGGTCG 585
Qy	481 CATACTTCAGGTTTTCGCGGAAAAAGTTCAAAAGTTAAAAATTAGAAAAATACAGGAA 540
Db	586 CATACTTCAGGTTTTCGAGGAAAAAGTTCAAAAGTTAAAAATTAGAAAAATATAAGAA 645
Qy	541 ATTATCGGCTTGATCCTGCTGACCGGTATTTTCATCGAGTGACTGTCGCGACAGACTT 600
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Db	706 TGCGAAACAGACGAGAAATATGTTCAAGCTATACATACATCAGCCATATTAGAGTATAT 765
Qy	661 TATAATGTTGGTAGCGTTGATTTCTACGTAATATGGAATAATCAACCTGGTTCAT 720
Db	766 TATAACGTTGGTAGCGTTGATTTTACGTAATATGGAATAATCAACCTGGTTCAGC 825
Qy	721 GAACCATCTGCTCTCATACGAAAGCCGTGAATATCTGACTGAGTCATAAATCATGAA 780
Db	826 GAACCATCTGCTCTCATACGAAAGCCGTGAATATCTGACTGAGTGTATAAACGTGAA 885
Qy	781 TGTGTTTAATTGGAACACCATGGAAGAAATATTTCAGCACTCCAAAACCAATTTCCAG 840
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Qy	841 TGCAGAGAGACACCTGTGTTGCGTTGATGGAATGCAAAAAGTTATCTGCTAGAGGC 900
Db	946 TGCAAAAGAGACACCTGTGTTGCGTTGAGTGAACGCTCAAAGTATCTGCTAAGGC 1005
Qy	901 GCATTTTATGACCGGTTGAAGCAATGCACCTTATGGCATTAACGAGGGATTAACCTT 960
Db	1006 TCATTTTATGTAACCTGTGTAATAAGATGCACCTTATGCCATTAACGAGGCATTAACCTG 1065
Qy	961 TAATTATTAACAAGTCAATGTACCAAAAATGTATCTATTGATGAATATTAAATGAAT 1020
Db	1066 TAATTGTAAACAATGAAAAATGTATA-AAATAATAATGAATAATGAACAGTCAAAAAAA 1124
Qy	1021 AAACGAACAGTCAAAATAAAAAAA 1048

Db	1125 AAAAAAAAAAAAAAAAAAAAAAAAAA 1152
RESULT 6	
AY566646	
LOCUS	
DEFINITION	
AY566646 948 bp mRNA linear INV 22-MAR-2004	
Polistes dominulus venom phospholipase A1 2 precursor mRNA, partial cds.	
ACCESSION	
AY566646	
VERSION	
AY566646.1 GI:45510888	
KEYWORDS	
SOURCE	
ORGANISM	
Polistes dominulus (European paper wasp)	
Polistes dominulus	
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Polistinae; Polistes.	
REFERENCE	
1 (bases 1 to 948)	
Moawad, T.I.S. and Hoffman, D.R.	
AUTHORS	
TITLE	
JOURNAL	
Direct Submission	
Submitted (05-MAR-2004) Pathology and Laboratory Medicine	
Department, Brody School of Medicine, East Carolina University, 600	
Moye Blvd., Greenville, NC 27858, USA	
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location/Qualifiers	
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Best Local Similarity 89.3%; Pred. No. 7.2e-143;	
Matches 843; Conservative 0; Mismatches 101; Indels 0; Gaps 0;	
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Qy	76 TTTAATGAGAAAGATATAGTATTCTATGTTTACTCAAGGAGATAAGCAGATGATTATT 135
Db	64 TTTAATGAGAAAGATATAGTATTGCTTACTCAAGGAGATAAAGCAATGATTATT 123
Qy	136 CTTAAGAAAGAACTTTAAGCAATTACGATCTGTTTACAAAGTCTACAAATATCAAAACAA 195
Db	124 CTTAAGAAAGAAATTTTAAAGAAATTACGATCTGTTTCAAAAATCTCAAAATATCACATCAA 183
Qy	196 GTTGTAATTTCTTATACATGGTTTCTTCAACTGGGAAATAATGAAAACCTTCTGCTATG 255
Db	184 ATTGCAATTTCTTATACATGGTTTCTTCAACTGGGAAATAAGAAAATTTGATGCAATG 243
Qy	256 TCGAAAGCTTTAATAGAAAAGATGATTTCTTGTAATTTCCGTCGACTGGAAGAAGGT 315
Db	244 GCGAAAGCTTTGATAGAAAATAGATAATTTCTTGTAATTTCCGTCGACTGGAAGAAGGT 303
Qy	316 GCTTGTAATGCTTTTGCTTCAACAAAGGATGCTTTGGGTTATTTCCAAAGCCGTTGAAAC 375
Db	304 GCTTGCAATGCTTTTGCTTCAACTAATGATGTTTGGGTTACTCCCAAGCCGTTGAAAC 363

OY	376	ACACGTCACGGTTGGAAAATTTGTAGCTGATTTTACAAAACTACTTGTAGAAAAATATATAA 	435
Db	364	ACAAGTCACGTTGAAAATATGTAGCTGATTTTACAAATATTATAGTAACAATATATAA 	423
OY	436	GTCGTGATATCAAAATATACGATTGATCGGGCATAGTTGGCGGCATACTTCAGGTTTT 	495
Db	424	GTCGCCATGTCCGAATATACGATTCGGCCATAGTTGGGTGGCATACTTCAGGTTTT 	483
OY	496	GCGGAAAAAGAAGTTCAAAGTTAAAAATTAGGAAATACAGAATAATTACGGGCTTGAT 	555
Db	484	GCAGGAAAAAGAAGTTCAAGGTTAAAAATTAGGAAATATTAAGGAAATAATCGGGCTTGAT 	543
OY	556	CCTGCTGGACCCTATTTTCATCGGAGTGACTGTCCGACAGACTTTGCCGTAACAGCGCA 	615
Db	544	CCTGCTGGACCCTCTTTTCTAACGATAAATGTCCAAACAGACTTTGGCAAAACAGCGCA 	603
OY	616	GAATATGTTCAAGTTATATACATACATCAATCATATTAGAGTAATTAATATGTTGGTAGC 	675
Db	604	GAATATGTTCAAGCTATACATACATCACCATATTAGAGTAATTAATTAACGTTGGTAGC 	663
OY	676	GTTGATTTCTACGTAATTATGAAAAAATCAACCTGGTTGCAATGAACCATCCTGCTCT 	735
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OY	736	CATACGAAAGCCGTGAATATCTGACTGAGTGCATAAACATGAATGTTGTTAATTGGA 	795
Db	724	CATACGAAAGCCGTGAATATCTGACTGAGTGTATAAAACGTGAATGTTGTTAATTGGA 	783
OY	796	ACACCATGGAAGAAATATTTACGACTCCAAAACCAATTTCCAGTGCAGAGAGACACC 	855
Db	784	ACACCATGGAAGAGTTATTTTAGACGCCCCAAAACCAATTTCTCAGTGCAGAAAGAGACACC 	843
OY	856	TGTGTTTGCCTTGATTTGAATGCAAAAAAGTTATCCTGCTAGAGCGCATTTTATGACCG 	915
Db	844	TGTGTTTGCCTTGACTGAAGTGAAGCTCAAGTTATCCTGCTAAGGCTCATTTTATGTACTT 	903
OY	916	GTTGAAGCAATGCACCTTATTTGCCATAACGAGGGGATTAACCT 959 	
Db	904	GTTGAAAAAGATGCACCTTATTTGCCATAACGAAAGGCATTTAACT 947 	

RESULT 7
AY566647
LOCUS
DEFINITION
AY566647 948 bp mRNA linear INV 22-MAR-2004
Polistes dominulus venom phospholipase A1 3 precursor mRNA, partial
cds.
ACCESSION
AY566647
VERSION
AY566647.1 GI:45510890
KEYWORDS
SOURCE
ORGANISM
Polistes dominulus (European paper wasp)
Polistes dominulus
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
Vespoidea; Vespidae; Polistinae; Polistes.
1 (bases 1 to 948)
REFERENCE
Moawad, T.I.S. and Hoffman, D.R.
AUTHORS
TITLE
Direct Submission
JOURNAL
Submitted (05-MAR-2004) Pathology and Laboratory Medicine
Department, Brody School of Medicine, East Carolina University, 600
Moye Blvd., Greenville, NC 27858, USA
FEATURES
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1. .948
Location/Qualifiers

CDS

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Best Local Similarity	89.1%;	Pred. No. 3.1e-142;		
Matches 841; Conservative	0;	Mismatches 103;	Indels 0;	Gaps 0;

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QY	76	TTTAATGAGAAAG	ATATAG	TATTTCT	ATGTTT	ACTCA	AGGAT	TAAG	CGAG	ATG	TATTTAT	T	135
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QY	136	CTTAGAAGAAAC	TTTA	CGAAT	TACG	ATCTG	TTTCA	AA	GTCA	CAAT	CA	AA	195
Db	124	CTTAGAAGAAAC	TTTA	AGAA	TATAC	GATCTG	TTTCA	AA	ATCT	CA	AA	TATCA	183
QY	196	GTTGATTTCTT	ATACAT	GTGTTT	CTTCTT	CACTG	GGAA	TATG	AAAA	CTTCG	TGCT	ATG	255
Db	184	ATTGCAATTTCT	TATACAT	GTGTTT	CTTCTT	CACTG	GGAA	TATG	AAAA	CTTCG	TGCA	ATG	243
QY	256	TCGAAAGCTTT	ATATAG	AAAA	GATG	ATTTCTT	GTATTT	CGGTC	GACTG	GAAG	AGGCT	315	
Db	244	GCAGAAAGCTT	TATAG	AAAA	TAGAT	ATTTCTT	GTATTT	CGGTC	GACTG	GAAG	AGGCT	303	
QY	316	GCTTGTAA	TGCTTTG	CTTCA	CA	AA	GATG	CTTTGG	GTATTTCC	AA	AGCCG	TGGA	375
Db	304	GCTTGTAA	TGCTTTG	CTTCA	CA	CTA	TATG	ATGTTTGG	GTATTTCC	CA	AGCCG	TGGA	363
QY	376	ACACGTCACG	TTGGA	AAAA	TTTGT	AGCTGA	TTTAC	AAAA	CTACTG	TG	AAAA	ATAT	435
Db	364	ACACGTCACG	TTGGA	AAAA	TATGT	AGCTGA	TTTAC	AAAA	ATAT	TAG	TGA	CAAT	423
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Db	424	GTGCGATGT	CGA	AATATAC	AGTTG	ATCGG	CA	TAGTTGG	GCGCA	T	CTTCA	G	483
QY	496	GCGGAAAA	AGAGTT	CA	AAA	GTTAA	AA	TTAG	GA	AAAA	TACA	AG	555
Db	484	GCAGAAAA	AGAGTT	CA	AA	GTTAA	AA	TTAG	GA	AAAA	TACA	AG	543
QY	556	CCTGCTGA	CCGTA	TTTTT	CAT	CGAG	TG	ACTG	TC	CGG	CAG	CA	615
Db	544	CCTGCTGA	CCGTA	TTTTT	CTA	ACG	AG	TAA	TG	TC	CAG	ATG	603
QY	616	GAATATGT	CA	AGTTAT	TAC	ATAC	ATCA	ATAT	TAG	AG	TATAT	TAA	675</

QY	916	GTGGAACCAATGCACCTTATGGCCATAACGAGGGGATTAAC	959
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DEFINITION	Polistes dominulus venom phospholipase A1 4 precursor mRNA, partial cds.		INV 22-MAR-2004
ACCESSION	AY566649		
VERSION	AY566649.1	GI:45510892	
KEYWORDS			
SOURCE	Polistes dominulus (European paper wasp)		
ORGANISM	Polistes dominulus		
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Polistinae; Polistes.		
AUTHORS	1 (bases 1 to 948)		
TITLE	Moawad,T.I.S. and Hoffman,D.R.		
JOURNAL	Submitted (05-MAR-2004) Pathology and Laboratory Medicine Department, Brody School of Medicine, East Carolina University, 600 Moye Blvd., Greenville, NC 27858, USA		
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Best Local Similarity	89.0%;	Pred. No. 6.3e-142;	
Matches 840;	Conservative 0;	Mismatches 104;	Indels 0; Gaps 0;
QY	16	GATGATTCGACGACATTTAGAAATGCTACCTGAAATAGAGCATGCTCCGATGTACT	75
Db	4	GATGATTCGACCACTTGAGAAATGGCACCTTGACAGAGCATCACTCCGATTGTACT	63
QY	76	TTTAATGAGAAAGATATAGTATTCTATGTTTACTCAAGGATTAAGCAGATGTAATT	135
Db	64	TTTAATGAGAAAGATATGAGCTACACGTTTACTCAAGGATTAACGAATGTATTATT	123
QY	136	CTTAAGAAAGAACTTTAAGCAATTACGATCTGTTTACAAGTCTACAATATCAAAACA	195
Db	124	CTTAAGAAAGAAATTTAAGAAATTACGATCTGTTTCAAAAATCTCAATATCATCAA	183
QY	196	GTTGATTTCTTATACATGTTTCTTCTTCAACTGGGAATAATGAAAATTGTTGCTATG	255
Db	184	ATTGCAATTCCTATACATGTTTCTTCTTCAACTGGGAATAACGAAAATTTGATGCAATG	243
QY	256	TCGAAAGCTTTAATAGAAAAGATGATTTTCTTGTAAATTCGGTGCAGTGAAGAGGGT	315
Db	244	GCGAAAGCTTTGATAGAAATAGATTAATTTCTTGTAAATTCGGTGCAGTGAAGAGGGT	303
QY	316	GCTTGTAAATGCTTTTCTTCAACAAGGATGCTTTGGTATTTCGAAGCCGTTGGAAC	375

Db	304	GCTTGCATGCTTTGCTTCAACTAATGATGTTTGGGTACTCCCAAGCCGTTGGAAC	363
Qy	376	ACACGTCACGTTGGAATAATTGTAGCTGATTTTACAAACTACTTGTAGAAAATATATAA	435
Db	364	ACACGTCACGTTGGAATAATATGTAGCTGATTTTACAAAATTATTAGTAGAACATATATAA	423
Qy	436	GTGCTGATATCAAAATATACGATTGATCGGGCATAGTTTGGGCGGCATACCTTCAGGTTT	495
Db	424	GTGCCGATGTGCAATATACGATTGATCGGCCATAGTTTGGGTGCGCATACCTTCAGGTTT	483
Qy	496	GCGGAAAAAGAGTTCAAAAGTTAAATTAGGAAAATACAAGGAATTATCGGCTTGAT	555
Db	484	GCAGGAAAAAGAGTTCAAGGTTAAATTAGGAAAATATAAGGAATAATCGGCTTGAT	543
Qy	556	CCTGCTGACCCGTATTTTCATCGGAGTGACTGTCCGACAGACTTTCGCTAACAGACGA	615
Db	544	CCTGCTGACCCGTATTTTCATCGGAGTGACTGTCCGACAGACTTTCGCTAACAGACGA	603
Qy	616	GAATATGTTCAAGTTATACATACATCAATCATATTAAGAGTATATTATATGTTGGTAGC	675
Db	604	GAATATGTTCAAGTTATACATACATCAATCAATTAAGAGTATATTATTAACGTTGGTAGC	663
Qy	676	GTTGATTTCTACGTGAATTATGAAAAATCACTGTTGCAATGAACCATCCTGCTCT	735
Db	664	GTTGATTTTCTACGTGAATTATGAAAAAGTCAACCTGTTGCAAGCAACCATCCTGCTCT	723
Qy	736	CATACGAAAGCCGTGAATAATCTGACTGAGTGCAATAAAACATGATGTTTAAATTGGA	795
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Qy	796	ACACCATGGAAGAAATATTTTCAGCACTCCAAAACCAATTTCCAGTGACAGAGACACC	855
Db	784	ACACCATGGAAGAGTTATTTAGCACGCCAAAATCAATTTCTCAGTGCAAAAAGACACACC	843
Qy	856	TGTGTTGCGTTGATGATGCAATGCAAAAAAGTTATCCTGCTAGAGCGCATTTTATGCAACG	915
Db	844	TGTGTTGCGTTGATGATGCAATGCAACGCTCAAAAGTTATCCTGCTAAAGGCTCATTTTATGTAACCT	903
Qy	916	GTTGAAGCAAAATGCACTTATTTGCCATAACGAGGGGATTAAACT	959
Db	904	GTTGAAGCAAAATGCACTTATTTGCCATAACGAGGCAATTAACCT	947
RESULT 9			
LOCUS	ARI62936	1050 bp	DNA linear PAT 17-OCT-2001
DEFINITION	Sequence 16 from patent US 6270763.		
ACCESSION	ARI62936		
VERSION	ARI62936.1	GI:16233392	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1050)		
AUTHORS	King, T. Piao.		
TITLE	Cloning and recombinant production of vespid venom phospholipases,		
JOURNAL	and immunological therapies based thereon		
FEATURES	Patent: US 6270763-A 16 07-AUG-2001;		
source	Location/Qualifiers		
	1..1050		
	/organism="Unknown"		
	/mol_type="unassigned DNA"		
ORIGIN			
Query Match	42.1%;	Score 441;	DB 6; Length 1050;
Best Local Similarity	67.0%;	Pred. No. 3.6e-76;	
Matches	665;	Conservative 0;	Mismatches 310; Indels 18; Gaps 2;
Qy	65	CGGATTGTTACTTTTAATGAGAAAGATATAGTATTCTATGTTTACTCAAGGATTAAGCGAG	124
Db	56	CCGATATGTCCTTTAGTAAATGATACAGTTAAGATGATTTTAAACCAAGGAAACCGAA	115

Qy	125	ATGGTATTATCTTAAGAAAGAACTTTAAGCAATTACGATCTGTTTACAAGCTACAA	184
Db	116	AACATGATTTTATACGCTAGTACAAATGAAACAGGCACAAATGAATTTAAGAGTCAATCA	175
Qy	185	TATCAAAACAAGTGTATTTCTTATACATGTTTCTTCAACTGGAAATATGAAAACT	244
Db	176	TAAACGTCACGTTGATTCATACGCGATGTTTACTTCTGTCGAACCGAAAAAAT	235
Qy	245	TCGTTGCTATGTCGAAAGCTTAAATAGAAAAAGATTTTCTTGAATTTCCGTCGACT	304
Db	236	TCGTTGCTATGTCAGAGGCTCTTATGCATACAGTGATTTTCTTATAATATGTCGATT	295
Qy	305	GGAAGAGCGTCTGTATGCTTTTGGCTTCAACAAAGATGCTTGGGTTATTCCAAAG	364
Db	296	GGCGGATGGCTGCTGTACTGATGAATACCAGGCTGAAGTATATGTTTATAAGGCTG	355
Qy	365	CCGTTGGAAAAACACAGCTCAGCTGGAAAAATTGTAAGCTGATTTTACAAAACTA	424
Db	356	CCGTTGGTAAATACACGCTTAGTTGAAATTTTATGCTATGATCGCAAGAAACTTGTAG	415
Qy	425	AAAAATATAAAGTGTGATATCAAAATATACGATGATCGGGCATAGTTGGCGCGCATA	484
Db	416	AACAATATAAAGTCCGATGACAAATATACGACTGTGGGACACAGTTTGGCGCACACA	475
Qy	485	CTTCAGGTTTTCGGGAAAGAACTTCAAAAGTTAAATTAGAAAAATACAAGAAATTA	544
Db	476	TTTCAGGTTTCGACAGCAAAAGAGTTCAAGAGTTAAATTAGAAAAATTTCTGAATTA	535
Qy	545	TCGGGCTTGATCCTGCTGACCGCTATTTTCATCGGAGTGACTGTCCGACAGACTTGGC	604
Db	536	TTGGGCTTGATCCTGCTGGGCTAGTTTCAAGAAAAATGATTTGCCGAGAGAACTGCG	595
Qy	605	TAAACAGCAGCAATATGTTCAAGTTATACATACATCAATCATATTAGAGTATATTATA	664
Db	596	AGACAGACGCACATTTATGACAAATTTTACATACATCGAGCAATTTAGGAACAGAGAA	655
Qy	665	ATGTTGGTAGCGTTGATTTCTACGTGAATTATGAAAAATCAACCTGGTGC-----	717
Db	656	CTCTTGGCACCGTCGATTTCTACATAATTAACGAAAGTAATCAACCCGTTGCAGATATA	715
Qy	718	--AATGAACCATCTGCTCTCATACGAAAGCCGTGAATAATCTGACTGAGTGCATAAAAC	775
Db	716	TTATTTGAGAAACTGCTCTCATACGAGAGCCGTGAATACTTTACCGAGTGCATAAGAC	775
Qy	776	ATGAATGTTGTTAATTGGAACACCATGGAAGAAATATTTACGACCTCAAAAACAATTT	835
Db	776	GCGAATGTTGTTAATTGGGCTCCC-----GCACTCCAAGAAATCCGACGCTGTTT	826
Qy	836	CCCACTGCAGAGAGACACTGTGTTTGGCTTGAATGCAAAAAGTTATCTCTGCTA	895
Db	827	CGAAGTCACAGAAACGAGCTGCTTTCGCTTGGAATTAACGCAAGAAATATCTTAAAA	886
Qy	896	GAGGCGCATTTTATGCAACCGGTTGAAGCAAAATGCACTTATGGCCATTAACGAGGGATT	955
Db	887	GGGCTCATTTTATGTACCGGTTGAAGCTGAAGCTCCATATTTGCAATTAACAACGGGAAA	946
Qy	956	AACTTTAATTATAACAAAAAGTCAATGTACACAAAAATGTATCTATTGATGAATATTAA	1015
Db	947	TAAATTAATTATATAAAAAAACATTACTATTGACAAAGTGCATTTGTTAATGATGAAA	1006
Qy	1016	TGAATTAACGAAACAGTCAAAATTAATAAAAAAAAAAAAAA	1048
Db	1007	TGAATTAATTAACGATTCAGAAAAAATAAAAAAAAAAAAAA	1039

RESULT 10
LOCUS ARI67265 1050 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 16 from patent US 6287559.
ACCESSION ARI67265
VERSION ARI67265.1 GI:17903034
KEYWORDS
SOURCE Unknown.

ORGANISM		Unknown.	
REFERENCE		Unclassified.	
AUTHORS		1 (bases 1 to 1050)	
TITLE		King,T.Piao.	
JOURNAL		Cloning and recombinant production of vespid venom hyaluronidases,	
FEATURES		and immunological therapies based thereon	
source		Patent: US 6287559-A 16 11-SEP-2001;	
ORIGIN		location/Qualifiers	
		1..1050	
		/organism="unknown"	
		/mol_type="unassigned DNA"	
Query Match		42.1%; Score 441; DB 6; Length 1050;	
Best Local Similarity		67.0%; Pred. No. 3.6e-76;	
Matches	665; Conservative	0; Mismatches 310; Indels 18; Gaps 2;	
Qy	65	CGGATTGCTATTTAATGAGAAAGATATAGTATTTCTATGTTTACTCAAGGATAGCGAG	124
Db	56	CCGATATGCCCTTTAGTATGATACAGTTAAGATGATTTTAAACAAGGAAACCGAA	115
Qy	125	ATGTTATTATTTTAAGAAAGAACTTTAACGAATTACGATCTGTTTACAAAGTCTACA	184
Db	116	AACATGATTTTATACGCTAGATACATGAACAGGCACAAATGAATTTAAGAAATCA	175
Qy	185	TATCAAAACAAGTGTATTTCTTATACATGTTTCTTCAACTGGGAATATGAAAACT	244
Db	176	TAAACGTCACGTTGATTTCAATACGAGTGTCTTCTGTCGAACCGAAAAAAT	235
Qy	245	TCGTTGCTATGTCGAAAGCTTAAATAGAAAAAGATGATTTTCTTGAATTTCCGTCGACT	304
Db	236	TCGTTGCTATGTCAGAGGCTCTTATGATACAGTGATTTTCTTATAATATGTCGATT	295
Qy	305	GGAAGAGGCTGCTGTAATGCTTTTGTCAACAAAGATGCTTGGTATTTCCAAG	364
Db	296	GGCGGATGGCTGCTGTACTGATGAATACCAGGCTGAAGTATATGTTTATAAGGCTG	355
Qy	365	CCGTTGGAACACACGCTCAGCTTGGAAATTTGTAGCTGATTTTCAAAAACACTGTTAG	424
Db	356	CCGTTGTAATACACGCTTAGTTGAAATTTTATGCTATGATGCAAAAGAACTTGTAG	415
Qy	425	AAAAATATAAAGTGTGATATCAAAATATACGATGATCGGGCATAGTTGGCGCGCATA	484
Db	416	AACAATATAAAGTCCGATGACAAATATACGACTGTGGGACACAGTTTGGCGCACACA	475
Qy	485	CTTCAGGTTTTCGGGAAAGAACTTCAAAAGTTAAATTAGAAAAATACAAGAAATTA	544
Db	476	TTTCAGGTTTCGACAGCAAAAGAGTTCAAGATTAATAATTTTCTGAATTA	535
Qy	545	TCGGGCTTGATCCTGCTGACCGCTATTTTCAATCGGAGTGACTGTCCGACAGACTTGGC	604
Db	536	TTGGGCTTGATCCTGCTGGGCTAGTTTCAAGAAAAATGATTTTCCGAGAAATCTGCG	595
Qy	605	TAAACAGCAGAAATATGTTCAAGTTATACATACATCAATCATTTAGAGTATATTATA	664
Db	596	AGACAGACGCACATTTATGTACAAATTTTACATACATCGAGCAATTTAGGAACAGAGAA	655
Qy	665	ATGTTGGTAGCGTTGATTTCTACGTGAATTAAGAAAAATCAACCTGGTGC-----	717
Db	656	CTCTTGGCACCGTCGATTTCTACATAATTAACGGAAGTAATCAACCCGTTGCAGATATA	715
Qy	718	--AATGAACCATCTGCTCTCATACGAAAGCCGTGAATAATCTGACTGAGTGCATAAAC	775
Db	716	TTATTTGAGAAACTGCTCTCATACGAGAGCCGTGAATAATCTTTACCGAGTGCATAAGAC	775
Qy	776	ATGAATGTTGTTAATTGGAACACCATGGAAGAAATATTTACGACCTCCAAAAACAATTT	835
Db	776	GCGAATGTTGTTAATTGGGCTCCC-----GCACTCCAAGAAATCCGACGCTGTTT	826
Qy	836	CCCACTGCAGAGAGACACTGTGTTTGGCTTGAATGCAAAAAGTTATCTCTGCTA	895
Db	827	CGAAGTCACAGAAACGAGTGTGCTTGGCTTGGAATTAACGCAAGAAATATCTTAAAA	886

Oy		896	GAGGCGCATTTTATGCACCCGGTTGAAGCAAAATGCACCCTTAATTGCCATAACGAGGGGATTA	955
Db		887	GGGGCTCATTATGTACCGGTTGAAGCTGAGCTCCATATTGCATAAACAACGGAAAA	946
Oy		956	AACCTTAATTATAAACAAAAGTCATGTACACAAAAATGTA(T)TGATGAATATATAA	1015
Db		947	TAA(T)TTAATTATATAAAAAAAAAACATTACTATTGCACACAAGTCATTTGTTAATGATGANA	1006
Oy		1016	TGAATAAACGAACAGTC(A)TAATAAAAAAAAAAAAAA	1048
Db		1007	TGAATAAATTACGATTCAGA(A)AAAAAAAAAAAAA	1039
RESULT 11				
LOCUS	I33765	1050 bp	DNA	linear PAT 06-FEB-1997
DEFINITION	Sequence 16 from patent US 5593877.			
ACCESSION	I33765			
VERSION	I33765.1	GI:	1824556	
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1050)			
TITLE	King,T.P. Nucleic acid and recombinant production of vespid venom hyaluronidase			
JOURNAL	Patent: US 5593877-A 16 14-JAN-1997;			
FEATURES	location/Qualifiers			
source	1..1050 <code>/organism=</code> "unknown" <code>/mol_type=</code> "unassigned DNA"			

Query Match	42.1%	Score 441	DB 6	Length 1050	
Best Local Similarity	67.0%	Pred. No. 3.6e-76			
Matches 665	Conservative 0	Mismatches 310	Indels 18	Gaps 2	
QY	65	CGGATTGTA	CTTTAATG	AAGAATATAGTATTTCTATGTTTACTCAAGGATTAAGCAG	124
DB	56	CCGTATGTC	CCCTTAGTA	TATGATACAGTTAAGATGATTTTTTAAACAAGGAAACCAG	115
QY	125	ATGCTATTAT	CTTAAGAA	AAGAACTTTAACGAATTCGATCTTTTACAAAGTCTACAA	184
DB	116	AACATGATTT	TATACGTA	GATACATGAAACAGGCACATGAATTTAAGAAAGTCAATCA	175
QY	185	TATCAAAACA	AGTTGTATT	CTTATACATGCTTCTTTCAACTGGGAATATGAAACT	244
DB	176	TAAACGTC	CAGTTGTAT	CATTACGCATGTTTACTCGTCTGCAACCGAAAAAATT	235
QY	245	TCGTTGCTAT	GTGGAAGCT	TTAATAGAAAAAGATGATTTCTGTATTTCCGTCGACT	304
DB	236	TCGTTGCTAT	GTCAAGGCT	CTTATGCATACAGGTGATTTCTTATATATGTCGATTT	295
QY	305	GGAAGAAGGG	GTCTGTATA	GTCTTTGCTTCAACAAGGATGCTTTGGGTATTCCAAAG	364
DB	296	GCGCGATGG	CTGTGTACT	GATGAATACCCAGGCTGGAATATGTTTATTAAGGCTG	355
QY	365	CCGTTGAAA	CACACAGCT	CAAGTTGGAATTTGTAGCTGATTTTACAAACTACTTGTAG	424
DB	356	CCGTTGTA	TACACGCTT	AGTTGGAATTTTATCGCTATGATCGCAAGAAACTGTAG	415
QY	425	AAAAATATA	AGTGCTGAT	TATCAATATACGATTGATCGGCATAGTTTGGCGGCATTA	484
DB	416	AACAATATA	AAAGTGCCG	ATGACAAATATACGACTGGTGGACACAGTTTGGCGGCACACA	475
QY	485	CTTCAGGTT	TGCGGAA	AAGAACTTCAAAAGTTTAAATTTAGAAAAATACAAAGAAATTA	544
DB	476	TTTCAGGTT	TCGCAAG	CAAAAGAGTTCAAGAGTTAAAAATTAGAAAAATTTCTGAAATTA	535
QY	545	TCGGGCTG	ATCCCTG	CTGACCCGTATTTTCATCGAGTGACTGTCGGACAGACTTTGCG	604
DB	536	TTGGGCTG	ATCCCTG	CTGAGCCTAGTTTCAAGAAAAATGATTTGTTCCGAGAGAACTTGGC	595

QY		605	TAA CAG ACG CAGA ATA TGT TCA AGT TTAT ATAC ATCAT CAAT CATATT TAGG AGT ATTATA	664
Db		596	AGACA GACGC ACATTA TGTA CAAATTTT ACATAC ATC GAGCAA TTTAGGA ACAGAGAAA	655
QY		665	ATGTTGGTAGCCGTGATTCTACGTAATTATGAAAAAATCAACTGGTTGC-----	717
Db		656	CTCTTGACACCGTCGATTCTACATMAATTAACGAAGTAATCAACC CGTTGCA GTATA	715
QY		718	--AATGA ACCAT CCTGCTCATACGAAAGCCGTGA AATATCTG ACTGAGTGCAT AAAC	775
Db		716	TTATTGAGAAACTGCTCTCATACGAGAGCCGTGA AATACTTACCGAGTGCAT AAGAC	775
QY		776	ATGAATGTTGTTAA TTGGAACACCATGGA GAATA TTTCA GCACTCCA AAACCA TTT	835
Db		776	GCGAATGTTGTTAA TTGGGGTCCC-----GCA GTCCA GAATCCGCA GCCTGTTT	826
QY		836	CCCAGTGCAGAGAGACACCTGTGTTTGCGTTGGA TTGAATGCCAAAAGTTATCCTGCTA	895
Db		827	CGAAGTGCACA GAAGAACGAGTGC GTTGGCGTTGAATTA AACGCAAGAAATATCTTAAAA	886
QY		896	GAGGCGCATTTTATGCACCCGGTTGAAGCAAA TGCACTTATTTGCCATTAACGAGGGGATTA	955
Db		887	GGGGCTCATTTTATGTATACCCGGTTGAAGCTGAAGCTCCATATTGCAATTAACAACGGGAAAA	946
QY		956	AAC TTATTTATTAACAAAAGTCAATGTACACA AAAATGTATCTATTGATGAATATTAA	1015
Db		947	TAA TTTAATTATATATAAAAAACATTA CTATTGACACA CAAGTGCA TTTGTTAATGATGAAA	1006
QY		1016	TGAATTAACGAACAGTCAAAATTA AAAAAAAAAAAAA 1048	
Db		1007	TGAATTAATTACGATTCAGAAAAA AAAAAAAAAAAAA 1039	

RESULT 12		136978		1050 bp		DNA		linear		PAT 13-MAY-1997	
LOCUS	136978										
DEFINITION	Sequence 16 from patent US 5612209.										
ACCESSION	136978										
VERSION	136978.1	GI:2084938									
KEYWORDS											
SOURCE	Unknown.										
ORGANISM	Unknown.										
REFERENCE	Unclassified.										
AUTHORS	1 (bases 1 to 1050)										
TITLE	King, T.P.										
JOURNAL	Cloning and recombinant production of vespid venom phospholipases, and immunological therapies based thereon										
FEATURES	Patent: US 5612209-A 16 18-MAR-1997;										
Source	Location/Qualifiers										
	1..1050										
	/organism="unknown"										
	/mol_type="unassigned DNA"										
ORIGIN											
Query Match	42.1%;	Score	441;	DB	6;	Length	1050;				
Best Local Similarity	67.0%;	Pred. No.	3.6e-76;								
Matches	665;	Conservative	0;	Mismatches	310;	Indels	18;	Gaps	2;		
QY	65	CGGATTGCTACTTTAATGAGAAAGATATAGTATTCTATGTTTACTCAAGGATTAAGCGAG	124								
DB	56	CCGTATGTCCCTTTAGTAATGATACAGTTAAGATGATTTTTTAAACAAGGAAAAACCGAA	115								
QY	125	ATGTATTATTCTTAAGAAAGAACTTTAAGAAATTAAGATCGATCTGTTTACAAAGTCTACAA	184								
DB	116	AACATGATTTTATACGCTAGATACATGAACAGCACATGAATTTAAGAGTCAATCA	175								
QY	185	TATCAAAACAAGTTGATTTCTTATACATGGTTCTTCAACTGGAAATATGAAGAACT	244								
DB	176	TAAACGTCCAGTTGATTCATTACGCAATGGTTTACTTCTGCTGCAACGAAAAAATT	235								
QY	245	TCGTGCTATGTCGAAAGCTTTAATAGAAAAAGATGATTTTCTGTATTTCCGTCGACT	304								

Db 236 TCGTTGCTATGTCAGAGGCTTTATGCATACAGGTATTTCTTATATATATGTCGATT 295
Qy 305 GGAAGAAGGCTGCTTGTATGCTTTTGTCTTCAACAAAGATGCTTTGGTTATTCAAAG 364
Db 296 GCGGATGCGCTGCTTGTACTGATGAATACCCAGGCTGAAGTATATGTTTATTAAGGCTG 355
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Db 356 CCGTTGGTAAATACACGCTTAGTTGGAATTTTATCGCTATGATCGCAAGAAACTTGTAG 415
Qy 425 AAAATATTAAGTGTGATATCAATATACGATTTGCGGCATAGTTGGCGCGCAT 484
Db 416 AACATATTAAGTCCCGATGACAAATATACGACTGGTGGACACAGTTTGGCGCACACA 475
Qy 485 CTTCAAGTTTTCGGGAAAAGAGTTCAAAAGTTAAATTAGAAAATACAGGAATTA 544
Db 476 TTTCAAGTTTCGACGGCAAAAGAGTTCAAGAGTTAAATTAGAAAATTTTCTGAATTA 535
Qy 545 TCGGCTTGATCCTGCTGACCGTATTTTCATCGAGTGACTGTCGACAGACTTTGCG 604
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Qy 605 TAAACAGCAGCAATATGTTCAAGTTATACATACATCAATCATATTAGAGTATATTATA 664
Db 596 AGACAGACGACATTAATGACAAATTTTACATACATCGAGCAATTTAGAACAGAGAA 655
Qy 665 ATGTTGGTAGCGTTGATTTTCTACGTGAATTTAGAAAATCAACCTGGTGC----- 717
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Qy 776 ATGAATGTTGTTAATTGGAACACCATGGAAGAAATATTTCAAGCACTCCAAAACCAATT 835
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Db 827 CGAAGTCACAAAGAAAGAGTGCCTTTGCGTTGAATTAACGCAAGAAATATCCTAAAA 886
Qy 896 GAGCGCATTTTATGACCGGTTGAAGCAAAATGCACTTATTGCCATTAACGAGGGATTA 955
Db 887 GGGGCTCATTTTATGTACCGGTTGAAGCTGAAGCTCCATATTGCAATTAACAACGGGAAA 946
Qy 956 AACTTTAATTATAAACAAGTCAATGTACACAAAATGTATCTATTGATGATATTAA 1015
Db 947 TAATTTAATTATATAAAAAACATTACTATTGACACAAGTGCAATTTGTTAATGATGAAA 1006
Qy 1016 TGAATAAACGACAGTCAAAATAAAAAAAA 1048
Db 1007 TGAATTAATTACGATTCAAGAAAAAAA 1039

RESULT 13
AR206926 1050 bp DNA linear PAT 20-JUN-2002
LOCUS AR206926 Sequence 16 from patent US 6372471.
DEFINITION AR206926
ACCESSION AR206926
VERSION AR206926.1 GI:21505676
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1050)
TITLE King,T.Piao.
Cloning and recombinant production of vespid venom enzymes, such as phospholipase and hyaluronidase, and immunological therapies based thereon

JOURNAL Patent: US 6372471-A 16 16-APR-2002;
FEATURES Location/Qualifiers
source 1..1050

/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 42.1%; Score 441; DB 6; Length 1050;
Best Local Similarity 67.0%; Pred. No. 3.6e-76;
Matches 665; Conservative 0; Mismatches 310; Indels 18; Gaps 2;

Qy 65 CGATTTGACTTTTAATGAGAAAGATATAGTATCTATGTTTACTCAAGGATAGCGAG 124
Db 56 CCGTATGTCCTTTAGTAAATGATACAGTTAAGATGATTTTTTTACAAAGGAAACCGGAA 115
Qy 125 ATGCTATTATCTTAAGAAAGAACTTTAACGAATTACGATCTGTTTACAAAGTCTACAA 184
Db 116 AACATGATTTTATACGCTAGATACAAATGAACAGGCACAAATGAATTTAAGAAATCA 175
Qy 185 TATCAAAACAAGTTGATTTCTTATACATGCTTCTTCAACTCGGAATTAATGAAACT 244
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Qy 245 TCGTTGCTATGCGAAAGCTTTAATAGAAAAGATGATTTTCTGTAATTTCGTCGACT 304
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Qy 305 GGAAGAAGGCTGCTGTAATGCTTTTGCTTCAACAAAGATGCTTTGGTATTTCCAAAG 364
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Qy 365 CCGTTGGAACACACGTCACGTTGGAATTTGTAAGTATTTAATACTACTGTTAG 424
Db 356 CCGTTGTAATACACGCTTAGTTGGAATTTTATCGCTATGATGCAAGAAACCTTGTAG 415
Qy 425 AAAATATTAAGTGTGATATCAAAATATACGATTGATCGGGCATAGTTGGCGCGCAT 484
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Qy 1016 TGAATAAACGACAGTCAAAATAAAAAAAA 1048

TITLE Cloning and recombinant production of vespid venom phospholipases,
and immunological therapies based thereon
JOURNAL Patent: US 6270763-A 26 07-AUG-2001;
FEATURES location/Qualifiers
source 1..1341
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 40.7%; Score 426.2; DB 6; Length 1341;
Best Local Similarity 66.9%; Pred.No.2.7e-73;
Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;

QY 64 CCGGATGTACTTTTAATGAGAAAGATATAGTATCTATGTTTACTCAAGGATAAGCGA 123
DB 156 CCAATATGTCCTTTAATCTGATACAGTTTCGATTAATTATTGAACAGGAAACCGA 215
QY 124 GATGTTATTTCTTAAGAAAGAACTTTAAGATTAAGATCTGTTTCAAAAGTCTACA 183
DB 216 AATCGTATCTTATACACTACAGACATTACAGATCATCTGAATTTAAGAAAAAACT 275
QY 184 ATATCAAAACAAGTGTATTTCTTATACATGTTTCTTCACTGGGAATAATGAAC 243
DB 276 ATACACAGTCCAGTGTATTCATTACACATGTTTACTTCACTGCAAGTGAACAAAT 335
QY 244 TTCGTGCTATGTCGAAGCTTTAATAGAAAAAGATGATTTCTTGTAAFTTCGTCGAC 303
DB 336 TTCAATAATTAGCAAAAGCTTTGGTAGATAAGATAACTATATGTTATCTCAATCGAT 395
QY 304 TGAAGAAGGGTGTGTTAATGCTTTGCTTCAAAGAGATGCTTGGGTATTCCAAA 363
DB 396 TGGCAGACGGCTGTTGTAATAAGAGTTAAAGTATTATTAATTATCTTACT 455
QY 364 GCCGTTGAAACACACGTCAGTTGAAAAATTGTAGCTGATTTTACAAACTACTGTA 423
DB 456 GCTGCTAGAAATACACGTTAGTTGACAAATATCGTACGATTAACCAAGAACTCGTA 515
QY 424 GAAAAATATAAGTGTGATATCAATATATACGATTCGGCATGTTGGCGCGCAT 483
DB 516 AAACACTATAAATCTCGATGGCAATATACGATTAATTGACATAGCTTAGAGCACAT 575
QY 484 ACTTCAGTTTTCGGGAAAGAGTTCAAAAGTTAAATTAGAAAAATACAAGAAATT 543
DB 576 GCTTCAGGTTTGCAGGCAAAAGTTCAGAGTTAAATTAGAAAAATATCTGAAATT 635
QY 544 ATCGGCTTGATCCTGCTGACCGTATTTTCATCGAGTGACTGTCGGACAGACTTGC 603
DB 636 ATTGGGCTTGATCCTGCTAGGCCCTTCGTTCAATCAATCATTTGTCGAAAGACTCTGC 695
QY 604 GTAACAGACGCAATATGTCAAGTTATACATCATCATATTAAGAGTATATTAT 663
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DB 816 TTTTCTCAGAGTTTGTCTCTCATTCGAGAGCCGTGATATACATGGCTGAGTCATAAA 875
QY 775 CATGAATGTGTTAATTGGAACACCATGGAAGAAATATTTCAGCACTCCAAAACCAATT 834
DB 876 CACGAATGTGTTAATTGGGATACC-----GAAGTCAAGAGTTTCGACGCTATT 926
QY 835 TCCCAAGTCAGAGAGACACCTGTGTTTGCCTGAGTTGAATGCAAAAAGTTATCTGCT 894
DB 927 TCGTCGTGACAAACAGAGTGCCTTTCGTTGATTAACGCAAGAGTATATACTAGT 986
QY 895 AGAGGCGCATTTTATGACCGGTTGAAGCAATGCACTTATTCATTAACGAGGGGATT 954
DB 987 AGAGGCTCATTTTATGTACCGGTTGAAGTACTGTTCTTTTGCAATAACAAGGGGAAG 1046

QY 955 AAATTTAATTATAACAAAGTCAATGTACACAAAAATGTATCTATTGATGAATATTAA 1014
DB 1047 ATAATTTAATAATAATAAAAAAGT-AAATTCCATTTCATCGAAATGCATTTGTTAATGTTGA 1105
QY 1015 ATGAATTAACGACAGTCAAAATAAAAA 1041
DB 1106 ATGAATAAATTACCATTTTAACAAATAA 1132

Search completed: April 28, 2005, 21:42:45
Job time : 4897 secs

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OM protein - protein search, using sw model

Run on: April 27, 2005, 12:34:46 ; Search time 168 Seconds
(without alignments)
736.686 Million cell updates/sec

Title: US-10-688-011-2

Perfect score: 1721

Sequence: 1 ICFLDSDSTFRNGTINRCM.....AFYAPVEANAPYCHNEGIKL 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1721	100.0	320	3	AAY84613	Aay84613 Amino aci
2	873.5	50.8	336	2	AAY25646	Aay25646 Vespula s
3	873.5	50.8	336	7	ADC34895	Adc34895 Wasp alle
4	866	50.3	317	2	AAR60599	Aar60599 Hornet ph
5	864	50.2	300	2	AAY25645	Aay25645 Vespula s
6	864	50.2	300	7	ADC34894	Adc34894 Wasp alle
7	856	49.7	300	2	AAR60603	Aar60603 Yellowjac
8	354	20.6	407	7	ADI23670	Adi23670 Mouse LPD
9	354	20.6	423	7	ADI23668	Adi23668 Mouse LPD
10	342.5	19.9	676	4	ABB62247	Abb62247 Drosophil
11	340.5	19.8	460	7	ADI23666	Adi23666 Human LPD
12	339	19.7	415	5	ABB78294	Abb78294 Amino aci
13	339	19.7	460	5	AAO14803	Aao14803 Phospholi
14	339	19.7	460	7	ABM79013	Abm79013 Human lip
15	339	19.7	481	5	AAO14804	Aao14804 Phospholi
16	339	19.7	489	5	AAU99734	Aau99734 Long form
17	339	19.7	489	7	ABM79014	Abm79014 Human lip
18	336	19.5	319	2	AAR30739	Aar30739 C-termina
19	336	19.5	452	2	AAR30737	Aar30737 Guinea pi
20	327	19.0	470	2	AAR30741	Aar30741 GPL(+) mu
21	326	18.9	319	2	AAR34292	Aar34292 C-termina
22	323.5	18.8	540	4	ABB61963	Abb61963 Drosophil
23	322	18.7	451	4	AAE10996	Aae10996 Human lip
24	322	18.7	451	4	AAE10996	Aae10996 Human lip
25	322	18.7	451	5	ABB06316	Abb06316 Human pho

26	322	18.7	451	6	ABU08952	Abu08952 Human nov
27	322	18.7	451	6	ADA83794	Ada83794 Human pho
28	322	18.7	451	7	ADI23676	Adi23676 Human LPD
29	322	18.7	451	7	ADI23674	Adi23674 Human LPD
30	322	18.7	451	8	ADR90482	Adr90482 Human pho
31	322	18.7	452	5	AAE17316	Aae17316 Human lip
32	320.5	18.6	451	7	ADI23672	Adi23672 Mouse LPD
33	318	18.5	432	2	AAR34294	Aar34294 HPL(-) mu
34	311.5	18.1	339	4	ABB62229	Abb62229 Drosophil
35	311.5	18.1	353	2	AAW59790	Aaw59790 Amino aci
36	311.5	18.1	353	3	AAB19176	Aab19176 A partial
37	311.5	18.1	354	2	AAW59791	Aaw59791 Amino aci
38	311.5	18.1	354	2	AAV41711	Aay41711 Human PRO
39	311.5	18.1	354	3	AAB44267	Aab44267 Human PRO
40	311.5	18.1	354	3	AAAB24413	Aab24413 Human PRO
41	311.5	18.1	354	3	AAB19177	Aab19177 Human LIP
42	311.5	18.1	354	4	AAU12371	Aau12371 Human PRO
43	311.5	18.1	354	4	AAB49892	Aab49892 Human PRO
44	311.5	18.1	354	4	AAB50912	Aab50912 Human PRO
45	311.5	18.1	354	6	ABO17815	Abol7815 Nove1 hum

ALIGNMENTS

RESULT 1	
AAY84613	
ID AAY84613	standard; protein; 320 AA.
AC AAY84613;	
DT 25-JUL-2000	(first entry)
DE Amino acid sequence of a Pol a venom phospholipase A1 polypeptide.	
KW Pol a venom; phospholipase A1; paper wasp; immune response; immunogen;	
KW vespid venom; allergen-specific allergy; hymenoptera venom;	
KW autoimmune condition; allergic condition; viral infection; HIV;	
KW human immunodeficiency virus; Herpes Simplex virus; papilloma virus.	
OS Polistes annularis.	
FH Key	Location/Qualifiers
FT Peptide	1..18
FT	/note= "signal peptide"
PN WO200018896-A1.	
XX 06-APR-2000.	
XX 01-OCT-1999;	99WO-US023211.
XX 01-OCT-1998;	98US-00166205.
XX (UYRQ) UNIV ROCKEFELLER.	
XX King TP;	
XX WPI; 2000-293139/25.	
XX N-PSDB; AAA12616.	
PT New nucleic acids encode enzymes of wasp venom, are useful to treat	
PT insect sting allergy or immune system-related disorders and differ from	
PT the genomic sequences in that introns have been removed.	
XX Claim 4; Fig 1; 72pp; English.	
XX The present sequence represents Pol a venom phospholipase A1 polypeptide,	
XX isolated from the paper wasp. The enzyme acts on phospholipid substrates,	
XX e.g. to hydrolyse fatty acids. The recombinant Polistinae venom is used	
XX to modulate an immune response to an immunogen in a mammal, particularly	
XX a vespid venom allergen-specific allergy, or allergy to other hymenoptera	
XX venom. Alternatively the venom enzyme is used to treat an immunologically	

CC affected disease or disorder, particularly a pathogenic disease or
CC disorder, an autoimmune condition, an allergic condition, especially an
CC allergy to hymenoptera venom, or a viral infection, especially human
CC immunodeficiency virus (HIV), Herpes Simplex virus or papilloma virus.
CC The enzyme is also useful to diagnose allergy
XX
SQ Sequence 320 AA;

Query Match 100.0%; Score 1721; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.5e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ICFLLDDSTFRNGTLNRGMSPDCTFNEKDIVFYVYSRDKRDGIILKKETLTNYDLFTKS 60
Db 1 ICFLLDDSTFRNGTLNRGMSPDCTFNEKDIVFYVYSRDKRDGIILKKETLTNYDLFTKS 60
OY 61 TISKQVFLIHGFLSTGNNEFVAMSKALIEKDFLVISVDWKKGACNAFASTKDALGYS 120
Db 61 TISKQVFLIHGFLSTGNNEFVAMSKALIEKDFLVISVDWKKGACNAFASTKDALGYS 120
OY 121 KAVGNTRHVGFVADFTKLVEKVKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKE 180
Db 121 KAVGNTRHVGFVADFTKLVEKVKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKE 180
OY 181 IIGLDPAGPYFHRSDCPDRLCVTDAEYVQVIHTSIILGVYNNVGSVDFVYNYGKNQPGCN 240
Db 181 IIGLDPAGPYFHRSDCPDRLCVTDAEYVQVIHTSIILGVYNNVGSVDFVYNYGKNQPGCN 240
OY 241 EPSCSHTKAVKYLTECIKHECCLIGTPWKKYFSTPKPISQCRGDTVCVGLNAKSYPARG 300
Db 241 EPSCSHTKAVKYLTECIKHECCLIGTPWKKYFSTPKPISQCRGDTVCVGLNAKSYPARG 300
OY 301 AFYAPVEANAPYCHNEGIKL 320
Db 301 AFYAPVEANAPYCHNEGIKL 320

RESULT 2
ID AAY25646
AAY25646 standard; protein; 336 AA.

AC AAY25646;
XX
DT 30-SEP-1999 (first entry)
XX
DE Vespuula sp. allergen 1352699 Ves V 1 protein fragment.
XX
KW Major histocompatibility complex; class II; desensitizing; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;
KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity; wasp.
XX
OS Vespuula sp.
XX
PN WO9934826-A1.
XX
PD 15-JUL-1999.
XX
PF 11-JAN-1999; 99WO-GB000080.
XX
PR 09-JAN-1998; 98GB-00000445.
PR 21-SEP-1998; 98GB-00020474.
XX
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI Larche M, Kay AB;
XX
DR WPI, 1999-458255/38.
XX
PT Desensitizing patients to polypeptide allergens.
XX

PS Example 6; Page 67; 117pp; English.

XX This invention describes a novel method of desensitizing a patient to a
CC polypeptide allergen and comprises administering to the patient a peptide
CC derived from the allergen where restriction to a MHC Class II molecule
CC possessed by the patient can be demonstrated for the peptide and the
CC peptide is able to induce a late phase response in an individual who
CC possesses the MHC Class II molecule. The methods can be used for
CC desensitizing patients to allergens present in e.g. grass, tree and weed
CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
CC Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
CC produce immunological vaccines which may be used to prevent and/or treat
CC conditions involving hypersensitivity to allergens. This sequence
CC represents a wasp (Vespuula sp.) allergen 1352699 Ves V 1
XX

SQ Sequence 336 AA;

Query Match 50.8%; Score 873.5; DB 2; Length 336;
Best Local Similarity 52.0%; Pred. No. 4.9e-79;
Matches 166; Conservative 55; Mismatches 87; Indels 11; Gaps 4;

OY 2 CPLLDDSTFRNGTLNRGMSPDCTFNEKDIVFYVYSRDKRDGIILKKETLTNYDLFTKST 61
Db 23 CYGHGDFLSYE--LDRG--PKCPFNSDVTYSIIETRENRRNDLYTLQTLONHPEFKKKT 77
OY 62 ISKQVFLIHGFLSTGNNEFVAMSKALIEKDFLVISVDWKKGACNAFASTKDALGYSK 121
Db 78 ITRPVVFITHGFTSSASETFNFINLAKALVDKDNVVISIDWQTACTNEAAGLKYLYYPT 137
OY 122 AVGNTRHVGFVADFTKLVEKVKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKEI 181
Db 138 AARNTRLVGQYIATITQKLVKHYKISMANTIRLIGHSLGAHAGSFAGKQVQELKGYSEI 197
OY 182 IGLDPAGPYFHRSDCPDRLCVTDAEYVQVIHTSIILGVYNNVGSVDFVYNYGKNQPGCN- 240
Db 198 IGLDPARPSFDSNHCSERLCETDAEYVQIHTSNYLGTETKLTGYDFYMANNGKNQPGCGR 257
OY 241 --EPSCSHTKAVKYLTECIKHECCLIGTPWKKYFSTPKPISQCRGDTVCVGLNAKSYPA 298
Db 258 FFSEVCSHRAVIYMAECIKHECCLIGIPRSK--SSQPISSCTKQECVCVGLNAKRYPS 314
OY 299 RGAFYAPVEANAPYCHNEG 317
Db 315 RGSFYVPVESTAPFCNNKG 333

RESULT 3
ID ADC34895
ADC34895 standard; protein; 336 AA.

AC ADC34895;
XX
DT 18-DEC-2003 (first entry)
XX
DE Wasp allergen VES V 1.
XX
KW allergen; antigen; hyporesponsive; desensitisation; immunomodulator;
KW gene therapy; wasp.
XX
OS Vespuula sp.
XX
PN WO2003047618-A2.
XX
PD 12-JUN-2003.
XX
PF 05-DEC-2002; 2002WO-GB005548.
XX
PR 05-DEC-2001; 2001US-0338385P.
XX

PA (CIRC-) CIRCASSIA LTD.
XX
PI Larche M, Ledger PW;
XX
XX WPI, 2003-523267/49.
DR
XX
XX Desensitizing an individual to a selected polypeptide antigen comprises
PT administering a composition containing polypeptide antigens in an amount
PT that generates a state of hyporesponsiveness to the antigen to allow
PT desensitization.
XX
XX
PS Disclosure; Page 37; 57pp; English.
XX
XX The invention relates to a novel method for desensitising an individual
CC to a selected polypeptide antigen. The method comprises administering a
CC composition that contains polypeptide antigens in an amount that
CC generates in the individual a state of hyporesponsiveness to the antigen
CC to allow desensitisation to one or more polypeptide antigens. The method
CC of the invention has immunomodulator activity, and may have a use in gene
CC therapy. The composition and method are useful in manufacturing a
CC medicament for desensitising an individual to a selected polypeptide
CC antigen or for generating in the individual a state of hyporesponsiveness
CC to the antigen to allow desensitisation to one or more polypeptide
CC antigens. The present sequence is used in the exemplification of the
CC invention.
SQ Sequence 336 AA;

Query Match	50.8%;	Score 873.5;	DB 7;	Length 336;
Best Local Similarity	52.0%;	Pred. No. 4.9e-79;		
Matches 166;	Conservative 55;	Mismatches 87;	Indels 11;	Gaps 4;

[illegible]

RESULT 4	
AA60599	
ID	AA60599 standard; protein, 317 AA.
XX	
AC	AA60599;
XX	
DT	25-MAR-2003 (revised)
DT	26-APR-1995 (first entry)
XX	
DE	Hornet phospholipase Dol mI.
XX	
KW	Hornet phospholipase; Vespid venom enzyme; VV;
KW	allergen-specific allergic condition; Dol mI.
XX	
OS	Dolichovespula maculata.
XX	

PN	WO9420623-A1.
XX	
PD	15-SEP-1994.
XX	
PF	10-MAR-1994; 94WO-US002629.
XX	
PR	11-MAR-1993; 93US-00031400.
PR	11-JAN-1994; 94US-00180209.
XX	
PA	(UVRQ) UNIV ROCKEFELLER.
XX	
PI	King TP;
XX	
DR	WPI; 1994-303030/37.
DR	N-PSDB; AAQ71520.
XX	
PT	Nucleic acid encoding vespid venom enzymes - used to produce polypeptides
PT	for diagnosis and treatment of vespid venom allergen-specific allergic
PT	conditions.
XX	
PS	Disclosure; Fig 1; 93pp; English.
XX	
CC	AAQ71520 is the cDNA sequence that codes for hornet phospholipase
CC	(AAR60599), a vespid venom (VV) enzyme. These enzymes were used to
CC	produce highly specific and individualised polypeptides for the diagnosis
CC	and the treatment of VV-specific allergen specific conditions. For
CC	therapy, the polypeptides or fragments can be administered by oral, nasal
CC	or parenteral routes. (Updated on 25-MAR-2003 to correct PN field.)
XX	
SQ	Sequence 317 AA;

Query Match	50.3%;	Score 866;	DB 2;	Length 317;
Best Local Similarity	54.5%;	Pred. No. 2.6e-78;		
Matches 162;	Conservative 42;	Mismatches 87;	Indels 6;	Gaps 2;

Qy	24	CTFNEKDIVFYVYSRDKRDGIIILKKETLTYNDLFYTSKTSISKQVFLIHGFLSTGNMNFV	83
Db	21	CPFSNDTVKMIPLTRENRKHDFFYLLDTMNRHNEFKSIIKRPFVFITHGFTSSATEKNFV	80
Qy	84	AMSKALIEKDDFLVISVDMWKGACNAFASTKDALGYSKAVGNTRHVGVADFTKLVEK	143
Db	81	AMSEALMHTGDFLIIMWDRMAACTDEYPLGKYMFKAAVGNTRLVGNFIAMIAKLVEQ	140
Qy	144	YKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYEIIIGLDPAGPYFHRSDCPDRLCVT	203
Db	141	YKVPMTNIRLVGHSLGAHISGFAGKRVQELKGKSEIIIGLDPAGPSFKNDCSERICET	200
Qy	204	DAEYQVVIHTSIIIGVYYNVGSDVFPYVNYGKNQPGCN--EPSCSHKAVKYLTECIIKHE	260
Db	201	DAHVQIILHTSSNLGTERTLGTVDIFYINNGSNQPGCRYIIIGETCSHTRAVKYFTECIIRE	260
Qy	261	CCLIGTPWKKYFSTPKPISQCRGDTCVCGLNAKSPARGAFYAPVEANAPYCHNEG	317
Db	261	CCLIGVPOSK--NPQVPSKCTRNECVCVGLNAKCPKRGSFYVPVEAEAPYCNNG	314

RESULT 5
 AAY25645
 ID AAY25645 standard; protein; 300 AA.
 XX
 AC AAY25645;
 XX
 DT 30-SEP-1999 (first entry)
 XX
 DE Vesputia sp. allergen 1709545 Ves M 1 protein fragment.
 XX
 KW Major histocompatibility complex; class II; desensitising; human;
 KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;
 KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
 KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
 KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
 KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity; wasp.
 XX

OS Vespu la sp.
XX
PN WO9934826-A1.
XX
PD 15-JUL-1999.
XX
PF 11-JAN-1999; 99WO-GB000080.
XX
PR 09-JAN-1998; 98GB-00000445.
PR 21-SEP-1998; 98GB-00020474.
XX
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
PI Larche M, Kay AB;
XX WPI; 1999-458255/38.
DR
XX
PT Desensitizing patients to polypeptide allergens.
XX
PS Example 6; Page 67; 117pp; English.
XX
CC This invention describes a novel method of desensitizing a patient to a
CC polypeptide allergen and comprises administering to the patient a peptide
CC derived from the allergen where restriction to a MHC Class II molecule
CC possessed by the patient can be demonstrated for the peptide and the
CC peptide is able to induce a late phase response in an individual who
CC possesses the MHC Class II molecule. The methods can be used for
CC desensitising patients to allergens present in e.g. grass, tree and weed
CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
CC Tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
CC produce immunological vaccines which may be used to prevent and/or treat
CC conditions involving hypersensitivity to allergens. This sequence
CC represents a wasp (Vespula sp.) allergen 1709545 Ves M 1
XX
SQ Sequence 300 AA;

Query Match 50.2%; Score 864; DB 2; Length 300;
Best Local Similarity 54.0%; Pred. No. 3.8e-78;
Matches 162; Conservative 51; Mismatches 79; Indels 8; Gaps 4;

OY 22 PDCTFNEKDIVFYVYSRDKRDGIIKKETLTNYDLFTKSTISKQVFLIHGFLSTGNEN 81
| | | | :
DB 2 PKCFPNSDVTSVIIETRENRRNDLYTLQTLQNHPEFKKTTITRPVFIITHGFTSSASEKN 61
OY 82 FVAMSKALIEKODFLVISVDMKKGAC-NAFASTKDALGYSKAVGNTRHVGFVADFTKLL 140
| :
DB 62 FINLAKALVDKDNVWVISIDWQTACTNEYPGLKYAY-YPTAASNTRLVGQYIATITOKL 120
OY 141 VEKYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKEIIGLDPAGPYFHRSDCPDRL 200
| :
DB 121 VKDYKISMANIRLIGHSLGAHVSGFAGKRVQELKLGKYSIITGLDPARPSFDSNHCSERL 180
OY 201 CVTDAEYVQVIHTSIILGVYVNVGSVDIFYVNYGKNQPGCN--EPSCSHTKAVKYLTCEI 257
| | | | | :
DB 181 CETDAEYVQIHTSNYLGTEKILGTVDIFYMNNGNKNNPGCGRFSEVCSHTRAVIYMAECI 240
OY 258 KHECCLIGTPWKKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317
| | | | | :
DB 241 KHECCLIGIPRSK--SSQPISRCTKQECVCVGLNAKKYPSRGSFYVPEVESTAPFCNNKG 297

RESULT 6
ADC34894
ID ADC34894 standard; protein; 300 AA.
XX
AC ADC34894;
XX
DT 18-DEC-2003 (first entry)
XX

DE Wasp allergen VES M 1.
XX
KW allergen; antigen; hyporesponsive; desensitisation; immunomodulator;
KW gene therapy; wasp.
XX
OS Vespu la sp.
XX
PN WO2003047618-A2.
XX
PD 12-JUN-2003.
XX
PF 05-DEC-2002; 2002WO-GB005548.
XX
PR 05-DEC-2001; 2001US-0338385P.
XX
PA (CIRC-) CIRCASSIA LTD.
PI Larche M, Ledger PW;
XX
DR WPI; 2003-523267/49.
XX
PT Desensitizing an individual to a selected polypeptide antigen comprises
PT administering a composition containing polypeptide antigens in an amount
PT that generates a state of hyporesponsiveness to the antigen to allow
PT desensitization.
XX
PS Disclosure; Page 37; 57pp; English.
XX
CC The invention relates to a novel method for desensitising an individual
CC to a selected polypeptide antigen. The method comprises administering a
CC composition that contains polypeptide antigens in an amount that
CC generates in the individual a state of hyporesponsiveness to the antigen
CC to allow desensitisation to one or more polypeptide antigens. The method
CC of the invention has immunomodulator activity, and may have a use in gene
CC therapy. The composition and method are useful in manufacturing a
CC medicament for desensitising an individual to a selected polypeptide
CC antigen or for generating in the individual a state of hyporesponsiveness
CC to the antigen to allow desensitisation to one or more polypeptide
CC antigens. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 300 AA;

Query Match 50.2%; Score 864; DB 7; Length 300;
Best Local Similarity 54.0%; Pred. No. 3.8e-78;
Matches 162; Conservative 51; Mismatches 79; Indels 8; Gaps 4;

OY 22 PDCTFNEKDIVFYVYSRDKRDGIIKKETLTNYDLFTKSTISKQVFLIHGFLSTGNEN 81
| | | | :
DB 2 PKCFPNSDVTSVIIETRENRRNDLYTLQTLQNHPEFKKTTITRPVFIITHGFTSSASEKN 61
OY 82 FVAMSKALIEKODFLVISVDMKKGAC-NAFASTKDALGYSKAVGNTRHVGFVADFTKLL 140
| :
DB 62 FINLAKALVDKDNVWVISIDWQTACTNEYPGLKYAY-YPTAASNTRLVGQYIATITOKL 120
OY 141 VEKYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKEIIGLDPAGPYFHRSDCPDRL 200
| :
DB 121 VKDYKISMANIRLIGHSLGAHVSGFAGKRVQELKLGKYSIITGLDPARPSFDSNHCSERL 180
OY 201 CVTDAEYVQVIHTSIILGVYVNVGSVDIFYVNYGKNQPGCN--EPSCSHTKAVKYLTCEI 257
| | | | | :
DB 181 CETDAEYVQIHTSNYLGTEKILGTVDIFYMNNGNKNNPGCGRFSEVCSHTRAVIYMAECI 240
OY 258 KHECCLIGTPWKKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317
| | | | | :
DB 241 KHECCLIGIPRSK--SSQPISRCTKQECVCVGLNAKKYPSRGSFYVPEVESTAPFCNNKG 297

RESULT 7
AAR60603
ID AAR60603 standard; protein; 300 AA.
XX
AC AAR60603;

```
XX
DT 25-MAR-2003 (revised)
DT 26-APR-1995 (first entry)
XX
DE Yellowjacket phospholipase.
XX
KM Yellowjacket phospholipase; vespid venom enzyme; VV;
KM allergen-specific allergic condition.
XX
OS Vesputia maculifrons.
XX
PN W09420623-A1.
XX
PD 15-SEP-1994.
XX
PF 10-MAR-1994; 94WO-US002629.
XX
PR 11-MAR-1993; 93US-00031400.
PR 11-JAN-1994; 94US-00180209.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
XX
PI King TP;
XX
DR WPI; 1994-303030/37.
DR N-PSDB; AAQ71523.
XX
PT Nucleic acid encoding vespid venom enzymes - used to produce polypeptides
PT for diagnosis and treatment of vespid venom allergen-specific allergic
PT conditions.
XX
PS Disclosure; Fig 5; 93pp; English.
XX
XX AAQ71523 is the cDNA sequence that codes for yellowjacket phospholipase
CC (AAR60603), a vespid venom (VV) enzyme. These enzymes were used to
CC produce highly specific and individualised polypeptides for the diagnosis
CC and the treatment of VV-specific allergen specific conditions. For
CC therapy, the polypeptides or fragments can be administered by oral, nasal
CC or parenteral routes. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 300 AA;

Query Match 49.7%; Score 856; DB 2; Length 300;
Best Local Similarity 53.2%; Pred. No. 2.4e-77;
Matches 159; Conservative 51; Mismatches 83; Indels 6; Gaps 2;

QY 22 PDCTFNEKDIYFVYVSRDKRDLGILKKEITLTNYDLFTKSTISKQVFLIHGFLSTGNNE 81
| | | | : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 PKCFPNSDVTISIETRENRNRLYTLQTNHPEFKKTIITRPVFTTHGFTSSASETN 61

QY 82 FVAMSKALIEKDFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGKFAVDFTKLLV 141
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 FINLAKALVDKDNVVISIDWQTAACTNEAAGLKLYYPFAARNTRLVGQYIATITQKLV 121

QY 142 EKYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKEITGLDPAGPYFHRSDCPDRLC 201
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 KHVKISMANTRLIGHSLGAHASGFAGKVOELKGKYSKITGLDPAAPSPFDSNHCSERLC 181

QY 202 VTDAEYVQVITHSIILGVYVNVGSVDFVYVNYGKNQPGCN--EPSCSHTKAVKYLTECIK 258
| | | | : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 ETDAEYVQIHTSNYLGTEKTLGTVDFYMNNGKNQPGCGRPFSEVCSHRAVIYMAECIK 241

QY 259 HECCLIGHTWKKYFSTPKPISQCRGPTCVCGLNAKSYPARGAFYAPVEANAPYCHNEG 317
| | | | : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 HECCLIGHTPKSK--SSQPISSCTKQECVCVGLNAKKYTSRGSFYVPVESTVPFCNNKG 297

RESULT 8
AD123670
ID AD123670 standard; protein; 407 AA.
XX
AC AD123670;
XX
```

```
DT 06-MAY-2004 (first entry)
XX
DE Mouse LDL #2.
XX
KM lipase; LPDL; LPDLR; lipase deficiency; atherosclerosis;
KM fatty liver disease; dyslipidaemia; hypercholesterolaemia;
KM hypertriglyceridaemia; mixed dyslipidaemia; lipid deficient state;
KM lipoprotein deficient state; mouse; enzyme.
XX
OS Mus sp.
XX
PN W02003055995-A2.
XX
PD 10-JUL-2003.
XX
PF 23-DEC-2002; 2002WO-CA001998.
XX
PR 21-DEC-2001; 2001US-0341786P.
PR 10-JAN-2002; 2002US-0346603P.
XX
PA (WENX/) WEN X.
PA (STEW/) STEWART A K.
PA (TSUI/) TSUI L.
PA (HEGE/) HEGELE R A.
XX
PI Wen X, Stewart AK, Tsui L, Hegele RA;
XX
DR WPI; 2003-569444/53.
DR N-PSDB; AD123669.
XX
PT Novel isolated LPDL or LPDLR lipase polypeptides, useful for identifying
PT substances that bind to the protein and which are useful for treating
PT diseases associated with lipase function e.g. atherosclerosis and
PT hypercholesterolemia.
XX
PS Claim 2; SEQ ID NO 6; 172pp; English.
XX
CC The invention relates to an isolated mammalian (e.g., human or mouse)
CC lipase polypeptide (polyp), e.g., LPDL (I) or LPDLR polyp (II). (I) or
CC (II) is useful for identifying substances which can bind with LPDL or
CC LPDLR polyp, and for identifying a compound that affects the binding of
CC LPDL or LPDLR polyp and an LPDL or LPDLR binding polyp. (I) or (II) or
CC their nucleic acid is useful for identifying a compound that affects LPDL
CC or LPDLR polyp activity or expression. (I) or (II) or their nucleic acid
CC is useful for detecting or monitoring a condition associated with
CC increased or decreased LPDL or LPDLR expression or activity in an animal,
CC where the condition is lipase deficiency, atherosclerosis, fatty liver
CC disease and dyslipidemias, such as hypercholesterolemia,
CC hypertriglyceridaemia, mixed (combined) dyslipidaemia, lipid or lipoprotein
CC deficient states, and/or any other tissue or plasma disorders of lipid or
CC lipoprotein metabolism. The nucleic acid is useful for diagnosing the
CC presence of or a predisposition for a disorder in a subject which
CC involves detecting a germline alteration in the nucleic acid in the
CC subject. An inhibitor is useful for modulating triglyceride activity by
CC inhibiting expression or activity of (I) or (II). The nucleic acid is
CC useful as a probe or primer. The present sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 407 AA;

Query Match 20.6%; Score 354; DB 7; Length 407;
Best Local Similarity 32.1%; Pred. No. 1.7e-26;
Matches 93; Conservative 44; Mismatches 109; Indels 44; Gaps 9;

QY 52 TNYDLFTKSTISKQVFLIHGFLSTGNNEFVA-MSKALIEKDFLVISVDWKKGACNAF 110
: | | | : : : : : : : : : : : : : : : : : : : : : : : :
Db 33 SNNSLNTFRNPAKKTWIIHGVRPFGSTPVMLSRFTKAFKQEDVNLIVDMNQATTFM 92

QY 111 ASTKDALGYSKAVGNTRHVGKFAVDFTKLVEK---YKVLISNIRLIGHSLGAHTSGFAG 167
| | | | : : : : : : : : : : : : : : : : : : : : : : : :
Db 93 -----YSRAVRNTRR-----VAEISRETLENLIGHSTLDNFHFIGMSLGAHISGFVG 140

QY 168 KEVQKLKGKYKEITGLDPAGPYFHRSDCPDRLCVTDAEYVQVITHSI-ILGVYVNVGSV 226
```


Db 141 ----KIFHGQLGRITGLDPAGPQFSRKPSNSRLYYTDAKFVDVIHTDIKSLGIGEPSGHI 196
QY 227 DFYVYGNQPGC-----NEPSCSHTKAVKYLTECIKHECCLIGTPMKKYESTPKPI 278
Db 197 DFYNGGKHQPGCPTSFSGTNFIKCDHQRAIYLFLLAFETSCNPFVSPCRSYKDYKNGL 256
QY 279 SQCRG---DTCVCVGLNAK-----SYPARGAFYAPVEANAPYC 313
Db 257 CVDGCLYKDCSPRLGNQAKLWKELKKTEEWPLRTTAFLDTSSQNPF 306

RESULT 9
AD123668
ID AD123668 standard; protein; 423 AA.
XX
AC AD123668;
XX
DT 06-MAY-2004 (first entry)
XX
DE Mouse LPDL #1.
XX
KW lipase; LPDL; LPDLR; lipase deficiency; atherosclerosis;
KW fatty liver disease; dyslipidaemia; hypercholesterolaemia;
KW hypertriglyceridaemia; mixed dyslipidaemia; lipid deficient state;
KW lipoprotein deficient state; mouse; enzyme.
XX
OS Mus sp.
XX
PN WO2003055995-A2.
XX
PD 10-JUL-2003.
XX
PF 23-DEC-2002; 2002WO-CA001998.
XX
PR 21-DEC-2001; 2001US-0341786P.
PR 10-JAN-2002; 2002US-0346603P.
XX
PA (WENX/) WEN X.
PA (STEM/) STEWART A K.
PA (TSUI/) TSUI L.
PA (HEGE/) HEGELE R A.
XX
PI Wen X, Stewart AK, Tsui L, Hegele RA;
XX
DR WPI; 2003-569444/53.
DR N-PSDB; AD123667.
XX
PT Novel isolated LPDL or LPDLR lipase polypeptides, useful for identifying
PT substances that bind to the protein and which are useful for treating
PT diseases associated with lipase function e.g. atherosclerosis and
PT hypercholesterolemia.
XX
PS Claim 2; SEQ ID NO 4; 172pp; English.
XX
CC The invention relates to an isolated mammalian (e.g., human or mouse)
CC lipase polypeptide (polyp), e.g., LPDL (I) or LPDLR polyp (II). (I) or
CC (II) is useful for identifying substances which can bind with LPDL or
CC LPDLR polyp, and for identifying a compound that affects the binding of
CC LPDL or LPDLR polyp and an LPDL or LPDLR binding polyp. (I) or (II) or
CC their nucleic acid is useful for identifying a compound that affects LPDL
CC or LPDLR polyp activity or expression. (I) or (II) or their nucleic acid
CC is useful for detecting or monitoring a condition associated with
CC increased or decreased LPDL or LPDLR expression or activity in an animal,
CC where the condition is lipase deficiency, atherosclerosis, fatty liver
CC disease and dyslipidemias, such as hypercholesterolemia,
CC hypertriglyceridemia, mixed (combined) dyslipidemia, lipid or lipoprotein
CC deficient states, and/or any other tissue or plasma disorders of lipid or
CC lipoprotein metabolism. The nucleic acid is useful for diagnosing the
CC presence of or a predisposition for a disorder in a subject which
CC involves detecting a germline alteration in the nucleic acid in the
CC subject. An inhibitor is useful for modulating triglyceride activity by
CC inhibiting expression or activity of (I) or (II). The nucleic acid is

CC useful as a probe or primer. The present sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 423 AA;
Query Match 20.6%; Score 354; DB 7; length 423;
Best Local Similarity 31.4%; Pred. No. 1.8e-26;
Matches 93; Conservative 45; Mismatches 110; Indels 48; Gaps 9;
QY 52 TNYDLFTKSTISKQVFLIHGFLSTGNNEFVA-MSKALIEKDDFLVISVDMKKACNAF 110
Db 33 SNNSLNTRFNPAKTIWTHIGYRPFGSTPWLISRFTKAFKQEDVNLIVDWNQATTFM 92
QY 111 ASTKDALGYSKAVGNTRHVGKFEVAD-FTKLVEKYKVLISNIRLIGHSLGAHTSGFAGKE 169
Db 93 -----YSRAVRNTRRYAEILRETIENLLI--HGASLDNFHFGMSLGAHISGFVG-- 140
QY 170 VQKLKLGKYKEIIGLDPAGPYFHRSDCPDRLCVTDAEYVQVIHTSI-ILGVYVNGSVDF 228
Db 141 --KIFHGQLGRITGLDPAGPQFSRKPSNSRLYYTDAKFVDVIHTDIKSLGIGEPSGHIDF 198
QY 229 YVYVGNQPGC-----NEPSCSHTKAVKYLTECIKHECCLIGTPMKKYESTPKPI 280
Db 199 YPNGGKHQPGCPTSFSGTNFIKCDHQRAIYLFLLAFETSCNPFVSPCRSYKDYKNGLCV 258
QY 281 CRGD-----TTCVCVGLNAK-----SYPARGAFYAPVEANAPYC 313
Db 259 DCGNLKYKDCSPRLGERSCVYLLGNQAKLWKELKKTEEWPLRTTAFLDTSSQNPF 314

RESULT 10
ABB62247
ID ABB62247 standard; protein; 676 AA.
XX
AC ABB62247;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 13533.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL06350.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 13533; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIFO at ftp.wifo.int/pub/published_pct_sequences
XX
SQ Sequence 676 AA;

Query Match 19.9%; Score 342.5; DB 4; Length 676;
Best Local Similarity 30.1%; Pred. No. 5e-25;
Matches 93; Conservative 41; Mismatches 106; Indels 69; Gaps 10;

OY 33 FVYV-----SRDKRDGILLKKETLTNYDLFTKSTISKQVFLIHGFLSTGNN 79
Db 73 FYLYTLQNPSTGGQIKATQDSIDGSFFNPQNPTR-----ITIHGMSNMYKD 118
OY 80 ENFVAMSKALIEKDFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGKFAVADFTKL 139
Db 119 GVNTRVADAMFQYGDYNNMIAVDWLRGR-----SLEYASSVAGAPGAGKKVAALVDF 169
OY 140 LVEKYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYEIIGLDPAQPYFHRSDCPDR 199
Db 170 LVEGYGMSLDLTLIVGFSLGAHVAGHTAQVNSGKVGK--VVGLDPASPLISYSNTEKR 226
OY 200 LCVTDAEYVOVIHTS-IILGVYNNVGSVDYVYNYGKNQPGCN--EPSCSHTKAVKYLTE 255
Db 227 LSSD DALYVESIQTNGA ILGFGQPIGKASFYMNNGRSQPGCGIDITGSCSHTKAVLYVE 286
OY 256 CIKHECCLIGTPWKKYFSTPKPISQCR-----GDT--CVCVGLNAKSYPARGAFY 303
Db 287 ALL-----WNNF-----PSIKCESSVDANKNNGNTYSSVFMGASINFPVAEGIFY 332
OY 304 APVEANAPY 312
Db 333 VPVNKESPY 341

RESULT 11

AD123666
ID AD123666 standard; protein; 460 AA.

AC AD123666;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human LPDL.
XX
KW lipase; LPDL; LPDLR; lipase deficiency; atherosclerosis;
KW fatty liver disease; dyslipidaemia; hypercholesterolaemia;
KW hypertriglyceridaemia; mixed dyslipidaemia; lipid deficient state;
KW lipoprotein deficient state; human; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003055995-A2.
XX
PD 10-JUL-2003.
XX
PF 23-DEC-2002; 2002WO-CA001998.
XX
PR 21-DEC-2001; 2001US-0341786P.
PR 10-JAN-2002; 2002US-0346603P.
XX
PA (WENX/) WEN X.
PA (STEW/) STEWART A K.
PA (TSUI/) TSUI L.
PA (HEGE/) HEGELE R A.
XX
PI Wen X, Stewart AK, Tsui L, Hegele RA;
XX
DR WPI, 2003-569444/53.
DR N-PSDB; AD123665.
XX
PT Novel isolated LPDL or LPDLR lipase polypeptides, useful for identifying

PT substances that bind to the protein and which are useful for treating
PT diseases associated with lipase function e.g. atherosclerosis and
PT hypercholesterolemia.
XX
PS Claim 2; SEQ ID NO 2; 172pp; English.

CC The invention relates to an isolated mammalian (e.g., human or mouse)
CC lipase polypeptide (polyp), e.g., LPDL (I) or LPDLR polyp (II). (I) or
CC (II) is useful for identifying substances which can bind with LPDL or
CC LPDLR polyp, and for identifying a compound that affects the binding of
CC LPDL or LPDLR polyp and an LPDL or LPDLR binding polyp. (I) or (II) or
CC their nucleic acid is useful for identifying a compound that affects LPDL
CC or LPDLR polyp activity or expression. (I) or (II) or their nucleic acid
CC is useful for detecting or monitoring a condition associated with
CC increased or decreased LPDL or LPDLR expression or activity in an animal,
CC where the condition is lipase deficiency, atherosclerosis, fatty liver
CC disease and dyslipidemias, such as hypercholesterolemia,
CC hypertriglyceridemia, mixed (combined) dyslipidemia, lipid or lipoprotein
CC deficient states, and/or any other tissue or plasma disorders of lipid or
CC lipoprotein metabolism. The nucleic acid is useful for diagnosing the
CC presence of or a predisposition for a disorder in a subject which
CC involves detecting a germline alteration in the nucleic acid in the
CC subject. An inhibitor is useful for modulating triglyceride activity by
CC inhibiting expression or activity of (I) or (II). The nucleic acid is
CC useful as a probe or primer. The present sequence is used in the
CC exemplification of the invention.

XX
SQ Sequence 460 AA;

Query Match 19.8%; Score 340.5; DB 7; Length 460;
Best Local Similarity 32.0%; Pred. No. 4.5e-25;
Matches 103; Conservative 43; Mismatches 107; Indels 69; Gaps 14;

OY 41 RDGIILKKETL----TNYD-----LFTKS-----TISKQVFLIHGFLSTGN----N 79
Db 34 RDLFTPRIETITIMYTRYNLNCAEPLFEQNNSLNVNFTQKTVWLHGYRPVGSIPLWL 93
OY 80 ENFVAMSKALIEKDFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGKFAVADFTKL 139
Db 94 QNFV---RILNEEDMNVIIVDMSRGATTFI-----YNRAVNTRKVAVSLSVH1KN 142
OY 140 LVEKYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYEIIGLDPAQPYFHRSDCPDR 199
Db 143 LL-KHGASLDNFHFIGVSLGAHISGFVG---KIFHGQLGRITGLDPAGPRFSRKPYSR 197
OY 200 LCVTDAEYVOVIHT-SIILGVYNNVGSVDYVYNYGKNQPGCNEP-----SCSHTKAV 250
Db 198 LDYTDAPVDVIHSDSNGLIGQEPGLGHIDFYPNGGNKQPGCPKSI FSGIOFIKCNHQRAY 257
OY 251 KYLTECIRHECCLIGTPWKKY--FSTPKPISQCR-----RGDTCVCGLNAKSY----- 296
Db 258 HLFMASLETNCNFTISPPCRSYKDYKT---SLCVDCCDFEKEKSCPR1GYQAKLFXGLVKE 313
OY 297 -----PARGAFYAPVEANAPYC 313
Db 314 RMEGRPLRTVFLDTSGTYPFC 335

RESULT 12

ABB78294
ID ABB78294 standard; protein; 415 AA.

AC ABB78294;
XX
DT 05-DEC-2002 (first entry)
XX
DE Amino acid sequence of lipid-associated molecule (LIPAM)-5.
XX
KW Human; lipid-associated molecule; LIPAM; cardiovascular disease;
KW atherosclerosis; hypertension; aneurysm; congestive heart failure;
KW angina pectoris; heart disease; lung disease; edema; emphysema;
KW bronchitis; gastrointestinal disease; nausea; peptic ulcer;
KW Crohn's disease; lipid metabolism; Fabry's disease; diabetes mellitus;

Key	Location/Qualifiers
FT Modified-site	18 /note= "potential glycosylation site"
FT Modified-site	27 /note= "potential phosphorylation site"
FT Modified-site	84 /note= "potential phosphorylation site"
FT Domain	106. .134 /note= "transmembrane domain"
FT Modified-site	135 /note= "potential phosphorylation site"
FT Modified-site	145 /note= "potential phosphorylation site"
FT Modified-site	151 /note= "potential phosphorylation site"
FT Modified-site	232 /note= "potential phosphorylation site"
FT Domain	278. .306 /note= "transmembrane domain"
FT Modified-site	304 /note= "potential phosphorylation site"
FT Modified-site	311 /note= "potential phosphorylation site"
FT Modified-site	351 /note= "potential glycosylation site"
FT Modified-site	371 /note= "potential phosphorylation site"
FT Modified-site	411 /note= "potential phosphorylation site"
PN WO200263005-A2.	
PD 15-AUG-2002.	
PF 06-FEB-2002; 2002WO-US003813.	
PR 06-FEB-2001; 2001US-0266910P.	
PR 16-MAR-2001; 2001US-0276855P.	
PR 16-MAR-2001; 2001US-0276891P.	
PR 28-MAR-2001; 2001US-0279760P.	
PR 13-APR-2001; 2001US-0283818P.	
PR 20-APR-2001; 2001US-0285405P.	
PA (INCY-) INCYTE GENOMICS INC.	
PI Das D, Yao MG, Arvizu C, Baughn MR, Lu Y, Hafalia AJA, Wallia NK, Griffin JA, Lu DAM, Yue H, Ding L, Townley DJ, Elliott VS; Forsythe I, Ramkumar J, Gandhi AR, Ison CH, Warren BA, Tang YT; Emerling BM, Honchell CD;	
PI WPI, 2002-627558/67.	
DR N-PSDB; ABV72131.	
PT New human lipid-associated molecules, useful for diagnosing, treating or preventing cardiovascular disorders (e.g. aneurysms), neurological disorders (e.g. Parkinson's disease) or cancers (e.g. leukemia or lymphoma).	
PS Claim 1; Page 134-135; 152pp; English.	
CC The present sequence represents a lipid-associated molecule (LIPAM). LIPAM polypeptides, polynucleotides and agonists are useful for treating a condition associated with decreased expression of functional LIPAM. The	

antagonist is useful for treating a disease associated with overexpression of functional LIPM. The anti-LIPM antibody is useful for diagnosing a condition or disease associated with the expression of LIPM. The polypeptides, polynucleotides, agonists and antagonists may also be used for preventing these diseases. These polypeptides, polynucleotides, agonists and antagonists are particularly useful for diagnosing, treating or preventing cardiovascular (e.g. atherosclerosis, hypertension, aneurysms, congestive heart failure, angina pectoris, or ischaemic or rheumatic heart disease), lung (e.g. oedema, emphysema or bronchitis) gastrointestinal (e.g. nausea, peptic ulcer or Crohn's disease), lipid metabolism (e.g. Fabry's disease, diabetes mellitus or hyperlipidaemia), autoimmune/inflammatory (e.g. acquired immunodeficiency syndrome (AIDS), anaemia, asthma, gout, pancreatitis or Crohn's disease), neurological (e.g. stroke, Alzheimer's disease, multiple sclerosis, Parkinson's disease, anxiety, schizophrenia or amnesia), metabolic (e.g. Addison's disease), developmental (e.g. Cushing's syndrome), endocrine or cell proliferative disorders (e.g. cancers including leukemia, lymphoma or sarcoma)

Query Match	19.7%;	Score 339;	DB 5;	Length 415;
Best Local Similarity	32.8%;	Pred. No. 5.6e-25;		
Matches 96;	Conservative 38;	Mismatches 107;	Indels 52;	Gaps 11;

```
QY      53 NYDLFTKSTISKQVFLIHGFLETCN---NENFVAMSKALIEKDPLVISVDWKKGACN 108
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db     18 NNSLNVNENTQOKTVMLIHGIRPVGSIPMLONFV---RLINBEDMNVIIVDWSRGATT 74
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```
QY      109 AFASTKDALGYSKAVGNTRHVGKFAVDFTKLVEKKYVLISNIRLIGHSIGAHTSGFAGK 168
      ||::||| ||| ||| ::|||::|||::|||::|||::|||::|||::|||::|||
Db      75 FI-----YNRAVKNTTRKVAASVSIHKNLL-KHGASIDNEHFIGVSLGAHISGFVG- 124
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QY      169 EVQKLKLGKRYKEIIIGLDPAGPYFPHRSDCPDRLCTVDAEYQVIHT-SIILGVYVNVGSSVD 2277
      125 --KIFHGQIGRITGLDPAGPFRFRRKPPYSRLDYDTDAKFVDVHIHSDSNGLGIOEPLGHID 1811
Db

```

QY 228 FVYNYGKQPGCN-----SCSHTKAVKYLTECIKHECCLIGTPMKKY--FSTPEP 277

182 FYPNGNGKQPGCPKSI FSGIOFIKCNHORAVHLEMASLETNCFISFPCCRSYKDYKT--- 238

Db

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QY      278 ISQC-----RGDTCVCGVLNAKSY-----PARGAFYAPVEANAPYC 313
      ||| : : : ||| : ||| : ||| : |||
Db      239 -SLCYDDCDFEKEKSCPRLGYOAKLFGVYKERMEGRPLRTVFELDTSGTYPC 290

```

RESULT 13
AA014803
ID AA014803 standard; protein; 460 AA.

AA014803; AC

DT 08-JUL-2002 (first entry)

Phospholipase A1 protein.

Phospholipase A1; phospholipase inhibitor; phospholipase antagonist;
phospholipase potentiator; cancer; blood diseases; wound.

Unidentified.

PN WO200231131-A1.

PD 18-APR-2002.

20-AUG-2001; 2001WO-JP007106.

PR 11-OCT-2000; 2000JP-00311015.

PA (MOCH) MOCHIDA PHARM CO LTD.

PI Arai H, Aoki J;

XX

DR WPI; 2002-362678/39.
DR N-PDSB; AAL42566.

XX New phospholipase A1 having substrate specificity for phosphatidic acid,
PT useful in diagnosis and screening inhibitors, antagonists and
PT potentiators for treating e.g. hypertension.

PS Claim 1; Fig 1-Fig 2; 60pp; Japanese.

CC The invention comprises the amino acid and coding sequence of the
CC phospholipase A1. The phospholipase A1 DNA and protein sequences of the
CC invention are useful in diagnosis and screening of phospholipase
CC inhibitors, antagonists and potentiators for drug compositions which can
CC be used in treating hypertension, cancer, blood diseases and wounds. The
CC present amino acid sequence represents the phospholipase A1 protein of
CC the invention

XX Sequence 460 AA;
SQ

Query Match 19.7%; Score 339; DB 5; Length 460;
Best Local Similarity 32.8%; Pred. No. 6.4e-25;

Matches 96; Conservative 38; Mismatches 107; Indels 52; Gaps 11

OY NYDLFTKSTITSKVFLIHGFLTGN---NENFVAMSKALLIEKDPLVISVDWKKGCACN 108
| | : ||||| : : ||| : : || || ||
DB 63 NNSLVNFNTQKTIVLHIGRYPVSIPMLQNfv--RLINNEEDMNVVVDMRGATT 119
| :||||| ::| :| :| :| ||||| |||
OY 109 AFASDKDALGYSAVGANTRHVGKEVAFTKLVEKYKVLISNRILIGHSLGAHTSGFAKG 168
| :|||::| :| :| :| :| ||||| |||
DB 120 FI-----YNRAVKPTRKNAVASLSVHIKNLL-KHGASLDNFHFIVGSLSGHISGFVG- 169
| :|||:||| :| :| :| :| ||||| |||
OY 169 EVOKLKLGKYEIIGLDPAGPYFHRSDCPDRLCTDAEYGVYIHT-SIILGVYYNGSVD 227
| :| :| ||||| || ||||| :| :| :|
DB 170 ---KIIFHQDGRITGLDPAGPRFSRKRPYSRLDYTDAKFYDVITHSDSNGLGIOEBLGHID 226
| :| :| ||||| :| :| :| :| :| :|
OY 228 FVYNYGKNQPGCNER-----SCSHTKAVKYLTEICIKHECLLIGTPWKXY--FSTPKP 277
| | ||| :| :| :| :| :| :| :| :|
DB 227 FYPNGNKRCPCPKSIIFSIOFIKCNHQRVAVHLFMASLETNCNFISPCRSYDIYT--- 283
| | :| :| :| :| :| :| :| :| :|
OY 278 ISQC-----RGDTVCVCGLNAXSY-----PARGAFFAPVEANAPYC 313
| | :| :| :| :| :| :| :| :| :|
DB 284 -SLCVDDCFPEKESCPRLGYQAELFKGVLEKERMEGRPRTTVFLDTSGTYPFC 335
| | :| :| :| :| :| :| :| :| :|

RESULT 14
ABMT79013 .
ID ABMT79013 standard; protein; 460 AA.
XX
AC ABMT79013;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human lipase.
KW Human; lipase; modulator; screening; cytostatic; antidiabetic;
KW neuroprotective; nootropic; anticonvulsant; antiParkinsonian;
KM antiasthmatic; anorectic; cardiac; vasotrophic; antiarrhythmic;
XX hypotensive; uteropathic; gene therapy.
OS Homo sapiens.
XX
PN WO2003072767-A2.
XX
PD 04-SEP-2003.
PF 26-FEB-2003; 2003WO-EP001940.
XX
PR 27-FEB-2002; 2002US-0359634P.
PR 12-MAR-2002; 2002US-0363101P.
PR 30-JUL-2002; 2002US-0399133P.
XX 15-AUG-2002; 2002US-0403360P.
PA (FARB) BAYER AG.

XX	PI	Liou J;
XX	DR	WPI; 2003-712728/67.
XX	DR	N-PSDB; ACF80618.
XX	PT	Human lipase polynucleotide and its encoded protein, useful for
XX	PT	identifying modulators of lipase activity and in gene therapy for
XX	PT	preventing or treating e.g. cancer, diabetes, Alzheimer's disease,
XX	PT	ischemia, asthma or obesity.
XX	PS	Claim 1; Fig 2; 114pp; English.
XX	CC	The present sequence is the protein sequence of human lipase. The
XX	CC	invention provides isolated polynucleotides which encode human lipase,
XX	CC	including the present sequence, as well as expression vectors, host cells
XX	CC	and methods of detecting the lipase polynucleotide and producing the
XX	CC	lipase polypeptide. The lipase polynucleotides and polypeptides are used
XX	CC	in claimed methods of screening for agents that decrease or regulate the
XX	CC	activity of the lipase. Such agents, or an expression vector containing a
XX	CC	lipase polynucleotide, can be used to modulate the activity of a lipase
XX	CC	in a disease, e.g. cancer, diabetes, a central nervous system disorder,
XX	CC	asthma, obesity, a cardiovascular disorder or a urological disorder
XX	CC	(claimed). The CNS disorder may include Alzheimer's disease, Parkinson's
XX	CC	disease or Huntington's disease. The cardiovascular disorder may include
XX	CC	myocardial infarction, ischaemia, arrhythmias or hypertension. The
XX	CC	urological disorder may include benign prostatic hyperplasia
XX	SO	Sequence 460 AA;
	Query Match	19.7%; Score 339; DB 7; Length 460;
	Best Local Similarity	32.8%; Pred. No. 6.4e-25;
	Matches	96; Conservative 38; Mismatches 107; Indels 52; Gaps 11;
Qy	53	NYDLFTKSTISKQVFLIHGFLSTGN---NENFVAMSKALIEKDFLVISVDWKKGACN 108
Db	63	NNSLNVNFNTQKKTWLIHGYPVSGISPLWLQNFV---RLLNEEDMNVIVDWSRGATT 119
Qy	109	AFASTKDALGYSKAVGNTRHVGKFAVADFTKLVEKRVKLISNIRLIGHSLGARTSGFAG 168
Db	120	FI-----YNRAVKNTRKVAVSLSVHIKNLL-KHGASLDNFHFIGVSLGAHISGFVG- 169
Qy	169	EVQKLKLGKYKEIIGLDPAGPYFHRSDCPDRLCVTDAEYVQVIHT-SIILGVYVNGSVD 227
Db	170	---KIFHGQLGRITGLDPAGPRFSRKPYPYSLDYDAKFVDVIHSDSNGLSIGQEPGLHID 226
Qy	228	FVYVYGNKQPGCNBP-----SCSHTKAVKYLTEICIKHECCCLIGTPMKY--FSTPRK 277
Db	227	FYPNGGNKQPGCPRKSI FSGIQFIKCNHQRVAHLEMASLETNCNFI SPCRSYKDYKT--- 283
Qy	278	ISQC-----RGDTCCVGLNAKSY-----PARGAFYAPVEANAPYC 313
Db	284	SLCVDCCDFKEKSCPRGLGYQAKLFKGVLKERMGRPLRTTVFLDTSGYTFFC 335
	RESULT 15	
	AAO14804	
ID	AAO14804	standard; protein; 481 AA.
XX	AC	AAO14804;
XX	DT	08-JUL-2002 (first entry)
XX	DE	Phospholipase A1-related protein.
XX	KW	Phospholipase A1; phospholipase inhibitor; phospholipase antagonist;
XX	XX	phospholipase potentiator; hypertension; cancer; blood diseases; wound.
OS		Unidentified.
XX		
PN		WO200231131-A1.
XX		
PD		18-APR-2002.

XX 20-AUG-2001; 2001WO-JP007106.
PF
XX 11-OCT-2000; 2000JP-00311015.
PR
XX (MOCH) MOCHIDA PHARM CO LTD.
PA
XX Arai H, Aoki J;
PI
XX WPI; 2002-362678/39.
DR
XX N-PSDB; AAL42567.
XX
PT New phospholipase A1 having substrate specificity for phosphatidic acid,
PT useful in diagnosis and screening inhibitors, antagonists and
PT potentiators for treating e.g. hypertension.
XX
XX
PS Disclosure; Page 46-50; 60pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequence of the
CC phospholipase A1. The phospholipase A1 DNA and protein sequences of the
CC invention are useful in diagnosis and screening of phospholipase
CC inhibitors, antagonists and potentiators for drug compositions which can
CC be used in treating hypertension, cancer, blood diseases and wounds. The
CC present amino acid sequence represents a phospholipase A1-related protein
XX
XX Sequence 481 AA;
SQ

Query Match	19.7%;	Score 339;	DB 5;	Length 481;
Best Local Similarity	32.8%;	Pred. No. 6.9e-25;		
Matches 96; Conservative	38;	Mismatches 107;	Indels 52;	Gaps 11;

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    :      :      :      :      :      :      :      :      :      :      :
Db 84 NNSLNVNENTQKTVLWLIHGYPVGSILPLMLQNFV--RIIINEEDMNVIIVDWSRGATT 140
    |      |      |      |      |      |      |      |      |      |      |
    :      :      :      :      :      :      :      :      :      :      :
QY 109 AFASTKDALGYSKAVGNTRHVGVKFDVDFTKLVLEKYYKVLISNIRLIGHSLGAHTSGFAGK 168
    |      |      |      |      |      |      |      |      |      |      |
    :      :      :      :      :      :      :      :      :      :      :
Db 141 FI-----YNRAVKNTRKVAVSLSVHIKNLL-KHGASLDNFHFIVGSIGAHTSGFVG- 190
    |      |      |      |      |      |      |      |      |      |      |
    :      :      :      :      :      :      :      :      :      :      :
QY 169 EVQKLKLGKYEIIGLDPAGPYFHRSDCPDRLCVTDAEYVOIHT-SIILGVYVNGSVD 227
    |      |      |      |      |      |      |      |      |      |      |
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Db 191 ---KIFHGQLGRITGLDPAGPRFRRKPPYRSLDYTDAKFVDVYIHSDNSGLGIOEPLGHID 247
    |      |      |      |      |      |      |      |      |      |      |
    :      :      :      :      :      :      :      :      :      :      :
QY 228 FVYVNYGKNQPGCNEP-----SCSHTKAVKYLTECIKHCECLIGTPWKRY--FSTPKP 277
    |      |      |      |      |      |      |      |      |      |      |
    :      :      :      :      :      :      :      :      :      :      :
Db 248 FYPNGGNKQPGCPSKISFSGIQFIKCHQRAVHLFMASLETJNCNFIISPPCRSYKDYKT--- 304
    |      |      |      |      |      |      |      |      |      |      |
    :      :      :      :      :      :      :      :      :      :      :
QY 278 ISQC-----RGDTCVCGVGLNAKSY-----PARGAFYAPVEANAPYC 313
    |      |      |      |      |      |      |      |      |      |      |
    :      :      :      :      :      :      :      :      :      :      :
Db 305 -SLCVDDCDCEKESCPRLGYQAKLFKGVLEKERMEGRPLRTTVFLDTSGTYPFC 356
    |      |      |      |      |      |      |      |      |      |      |
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Search completed: April 27, 2005, 12:49:59
Job time : 171 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 27, 2005, 12:43:59 ; Search time 44 Seconds
(without alignments)
542.902 Million cell updates/sec

Title: US-10-688-011-2

Perfect score: 1721
Sequence: 1 ICFLLDDSTFRNGTLNRGM.....AFYAPVEANAPYCHNEGIKL 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1721	100.0	320	3 US-09-166-205B-64	Sequence 64, Appl
2	1721	100.0	320	4 US-09-806-658-2	Sequence 2, Appli
3	866	50.3	317	1 US-08-180-209B-17	Sequence 17, Appl
4	866	50.3	317	1 US-08-385-745-17	Sequence 17, Appl
5	866	50.3	317	3 US-08-485-388-17	Sequence 17, Appl
6	866	50.3	317	3 US-08-474-853-17	Sequence 17, Appl
7	866	50.3	317	3 US-09-166-205B-17	Sequence 17, Appl
8	866	50.3	317	4 US-09-806-658-7	Sequence 7, Appli
9	866	50.3	317	5 PCT-US94-02629-17	Sequence 17, Appl
10	856	49.7	300	1 US-08-180-209B-27	Sequence 27, Appl
11	856	49.7	300	1 US-08-385-745-27	Sequence 27, Appl
12	856	49.7	300	3 US-08-485-388-27	Sequence 27, Appl
13	856	49.7	300	3 US-08-474-853-27	Sequence 27, Appl
14	856	49.7	300	4 US-09-806-658-8	Sequence 8, Appli
15	856	49.7	300	5 PCT-US94-02629-27	Sequence 27, Appl
16	849	49.3	315	3 US-09-166-205B-27	Sequence 27, Appl
17	434	25.2	121	1 US-08-180-209B-22	Sequence 22, Appl
18	434	25.2	121	1 US-08-385-745-22	Sequence 22, Appl
19	434	25.2	121	3 US-08-485-388-22	Sequence 22, Appl
20	434	25.2	121	3 US-08-474-853-22	Sequence 22, Appl
21	434	25.2	121	3 US-09-166-205B-22	Sequence 22, Appl
22	434	25.2	121	5 PCT-US94-02629-22	Sequence 22, Appl
23	311.5	18.1	353	3 US-08-985-492-4	Sequence 4, Appli
24	311.5	18.1	354	3 US-08-985-492-6	Sequence 6, Appli
25	310.5	18.0	345	3 US-08-985-492-10	Sequence 10, Appl
26	310.5	18.0	500	3 US-08-985-492-8	Sequence 8, Appli
27	309	18.0	449	4 US-09-949-016-8115	Sequence 8115, Ap

28	309	18.0	465	3 US-08-985-492-15	Sequence 15, Appl
29	309	18.0	465	4 US-09-411-132A-6	Sequence 6, Appli
30	305.5	17.8	475	4 US-09-054-272-40	Sequence 40, Appl
31	297.5	17.3	467	4 US-09-411-132A-4	Sequence 4, Appli
32	295	17.1	472	3 US-08-985-492-13	Sequence 13, Appl
33	293.5	17.1	469	4 US-09-411-132A-5	Sequence 5, Appli
34	292	17.0	467	4 US-09-411-132A-3	Sequence 3, Appli
35	289.5	16.8	467	4 US-09-411-132A-10	Sequence 10, Appl
36	288.5	16.8	473	4 US-09-411-132A-8	Sequence 8, Appli
37	287.5	16.7	467	4 US-09-411-132A-9	Sequence 9, Appli
38	285.5	16.6	392	4 US-09-513-999C-4156	Sequence 4156, Ap
39	282.5	16.4	473	4 US-09-411-132A-7	Sequence 7, Appli
40	278	16.2	499	3 US-08-985-492-14	Sequence 14, Appl
41	278	16.2	499	4 US-09-949-016-5906	Sequence 5906, Ap
42	278	16.2	502	4 US-09-949-016-10424	Sequence 10424, A
43	271.5	15.8	284	4 US-09-270-767-43145	Sequence 43145, A
44	250.5	14.6	389	4 US-09-270-767-32291	Sequence 32291, A
45	250.5	14.6	389	4 US-09-270-767-47508	Sequence 47508, A

ALIGNMENTS

RESULT 1
US-09-166-205B-64
; Sequence 64, Application US/09166205B
; Patent NO. 6372471
; GENERAL INFORMATION:
; APPLICANT: Te Piao KING
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES,
; TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL
; FILE REFERENCE: 2313/OF138US
; CURRENT APPLICATION NUMBER: US/09/166,205B
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 64
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Polistes annularis
; US-09-166-205B-64

Query Match	100.0%;	Score 1721;	DB 3;	Length 320;
Best Local Similarity	100.0%;	Pred. No. 5.6e-183;		
Matches	320;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	ICFLLDDSTFRNGTLNRGMSPDCTFNEKDIVFYVYSRDKRDGIIKKETLTNYDLFTKS	60	
Db	1	ICFLLDDSTFRNGTLNRGMSPDCTFNEKDIVFYVYSRDKRDGIIKKETLTNYDLFTKS	60	
QY	61	TISKQVVFLLHGFLSTGNNEFVAMSKALIEKDDFLVISVDWKGACNAFASTYDALGYS	120	
Db	61	TISKQVVFLLHGFLSTGNNEFVAMSKALIEKDDFLVISVDWKGACNAFASTYDALGYS	120	
QY	121	KAVGNTRHVGKFEVADFTKLVKKYKVLISNIRLIGHSIGAHTSGFAGKEVQKLKGKYKE	180	
Db	121	KAVGNTRHVGKFEVADFTKLVKKYKVLISNIRLIGHSIGAHTSGFAGKEVQKLKGKYKE	180	
QY	181	IIGLDPAGPYFHRSDCPDRLCTDAEYVQVHTSIILGVYVNGSVDFYVNYGKNQPGCN	240	
Db	181	IIGLDPAGPYFHRSDCPDRLCTDAEYVQVHTSIILGVYVNGSVDFYVNYGKNQPGCN	240	
QY	241	EPSCSHTRKAVKYLTECIKHECCILGTPWKYFSTPKPISQCRGDTVCVGLNAKSYPARG	300	
Db	241	EPSCSHTRKAVKYLTECIKHECCILGTPWKYFSTPKPISQCRGDTVCVGLNAKSYPARG	300	
QY	301	AFYAPVEANAPYCHNEGIKL 320		
Db	301	AFYAPVEANAPYCHNEGIKL 320		

RESULT 2

US-09-806-658-2
; Sequence 2, Application US/09806658
; Patent No. 6652851
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF POLISTINAE VENOM ENZYMES, S
; TITLE OF INVENTION: PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BAS
; FILE REFERENCE: 2313/1F138-US1
; CURRENT APPLICATION NUMBER: US/09/806,658
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Polistes annularis
US-09-806-658-2

Query Match 100.0%; Score 1721; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.6e-183;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICFLDDSTFRNGTLNRGMSPDCTFNEKDIVFYVYSRDKRGGIILKKEITLNYDLFTKS 60
DB 1 ICFLDDSTFRNGTLNRGMSPDCTFNEKDIVFYVYSRDKRGGIILKKEITLNYDLFTKS 60
QY 61 TISKQVFLIHGFLSTGNNEFVAMSKALIEKDDFLVISDWKKGACNAFASTKDALGYS 120
DB 61 TISKQVFLIHGFLSTGNNEFVAMSKALIEKDDFLVISDWKKGACNAFASTKDALGYS 120
QY 121 KAVGNTRHVGEKVFADFTKLVEKYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKE 180
DB 121 KAVGNTRHVGEKVFADFTKLVEKYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKE 180
QY 181 IIGLDPAQPYFHRSDCPDRLCVTDAEYVQVIHTSIILGVYVNVGSVDFYVNYGKNQPGCN 240
DB 181 IIGLDPAQPYFHRSDCPDRLCVTDAEYVQVIHTSIILGVYVNVGSVDFYVNYGKNQPGCN 240
QY 241 EPSCSHTKAVKYLTECIKHECCILGTPWKYFSTPKPISQCRGDTVCVCGINAKSYPARG 300
DB 241 EPSCSHTKAVKYLTECIKHECCILGTPWKYFSTPKPISQCRGDTVCVCGINAKSYPARG 300
QY 301 AFYAPVEANAPYCHNEGIRL 320
DB 301 AFYAPVEANAPYCHNEGIRL 320

RESULT 3

US-08-180-209B-17
; Sequence 17, Application US/08180209B
; Patent No. 5593877
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
; TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED
; TITLE OF INVENTION: THEREON
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/180,209B
; FILING DATE: 11-JAN-1994

CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/031,400
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-074 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-180-209B-17

Query Match 50.3%; Score 866; DB 1; Length 317;
Best Local Similarity 54.5%; Pred. No. 1e-87;
Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2;

QY 24 CFNEKDIVFYVYSRDKRGGIILKKEITLNYDLFTKSTISKQVFLIHGFLSTGNNEFV 83
DB 21 CPEFNDTVKMIFLTRENRKHDFTYTLDTMNRHNEFKSIIKRPVFIHTGFTSSATEKNFV 80
QY 84 AMSKALIEKDDFLVISDWKKGACNAFASTKDALGYSKAVGNTRHVGEKVFADFTKLVEK 143
DB 81 AMSEALMHTGDFLLINVDWRMAACTDEYPLGLKMYFYKAAVGNTRLVGNFIAMIAKLVEQ 140
QY 144 KYVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKEIIGLDPAQPYFHRSDCPDRLCVT 203
DB 141 KYVPMTNIRLVGHSLSGAHISGFAGKRVQELKGFSEIIGLDPAQPYFHRSDCPDRLCVT 200
QY 204 DAEVQVIHTSIILGVYVNVGSVDFYVNYGKNQPGCN--EPSCSHTKAVKYLTECIKHE 260
DB 201 DAHYVQILHTSSNLGTERLTGLTVDFYINNGSNQPGCRYIIGETCSHTRAVKYFTECIRRE 260
QY 261 CCLIGTPWKYFSTPKPISQCRGDTVCVCGINAKSYPARGAFYAPVEANAPYCHNEG 317
DB 261 CCLIGVPOSK--NPQDVSKCTRNECVCVGINAKKYPKRGSFYVPEABAPYCNNG 314

RESULT 4

US-08-385-745-17
; Sequence 17, Application US/08385745
; Patent No. 5612209
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
; TITLE OF INVENTION: Based Thereon
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,745
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/031,400

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 3288-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-385-745-17

Query Match 50.3%; Score 866; DB 1; Length 317;
Best Local Similarity 54.5%; Pred. No. 1e-87;
Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2;

QY 24 CTFNEKDIVFYVSRDKRDGIIKKETLTNYDLFTKSTISKQVFLIHGFLSTGNNEFV 83
DB 21 CPFSNDTVKMIFLTRENKHDFTYLTDMNRHNEFKSIIKRPVFIITHGFTSSATEKNFV 80
QY 84 AMSKALIEKDDFLVISVDWKKGACNAPASTKDALGYSKAVGNTRHVGKFNADFTKLVEK 143
DB 81 AMSEALMHTGDFLLIMVDMRMACTDEYRGLKMFYKAAVGNTRLVGNFIAMIAKLVEQ 140
QY 144 YKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKEIIGLDPAGPYFHRSDCPDRLCVT 203
DB 141 YKVPMTNIRLVGHSLSGAHISGFAGKRVQELKLGKFSIIGLDPAGPSFKNDCSERICET 200
QY 204 DAEYVQVHTSIILGVYVNVGSVDIFYVNYGKNQPGCN--EPSCSHTKAVKYLTECIKHE 260
DB 201 DAHYVQILHTSSNLGTERLTGTVDIFYINNQSNOGCRYIIGETCSHTRAVKYFTECIRRE 260
QY 261 CCLIGTPWKRYSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317
DB 261 CCLIGVPQSK--NPQPVSKCTRNECVCGVLAACKYPRKGSFYVPEAEAPYCNNG 314

RESULT 5

US-08-485-388-17
Sequence 17, Application US/08485388
Patent No. 6270763
GENERAL INFORMATION:
APPLICANT: King, Te Piao
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
TITLE OF INVENTION: Based Thereon
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,388
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/385,745
FILING DATE: 08-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/031,400
FILING DATE: 11-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 FWCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-388-17

Query Match 50.3%; Score 866; DB 3; Length 317;
Best Local Similarity 54.5%; Pred. No. 1e-87;
Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2;

QY 24 CTFNEKDIVFYVSRDKRDGIIKKETLTNYDLFTKSTISKQVFLIHGFLSTGNNEFV 83
DB 21 CPFSNDTVKMIFLTRENKHDFTYLTDMNRHNEFKSIIKRPVFIITHGFTSSATEKNFV 80
QY 84 AMSKALIEKDDFLVISVDWKKGACNAPASTKDALGYSKAVGNTRHVGKFNADFTKLVEK 143
DB 81 AMSEALMHTGDFLLIMVDMRMACTDEYRGLKMFYKAAVGNTRLVGNFIAMIAKLVEQ 140
QY 144 YKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKEIIGLDPAGPYFHRSDCPDRLCVT 203
DB 141 YKVPMTNIRLVGHSLSGAHISGFAGKRVQELKLGKFSIIGLDPAGPSFKNDCSERICET 200
QY 204 DAEYVQVHTSIILGVYVNVGSVDIFYVNYGKNQPGCN--EPSCSHTKAVKYLTECIKHE 260
DB 201 DAHYVQILHTSSNLGTERLTGTVDIFYINNQSNOGCRYIIGETCSHTRAVKYFTECIRRE 260
QY 261 CCLIGTPWKRYSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317
DB 261 CCLIGVPQSK--NPQPVSKCTRNECVCGVLAACKYPRKGSFYVPEAEAPYCNNG 314

RESULT 6

US-08-474-853-17
Sequence 17, Application US/08474853
Patent No. 6287559
GENERAL INFORMATION:
APPLICANT: King, Te-piao
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,853
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/180,209
FILING DATE: 11-JAN-1994

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/031,400
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-074 CIPB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-474-853-17

```

Query Match	50.3%;	Score 866;	DB 3;	Length 317;
Best Local Similarity	54.5%;	Pred. No. 1e-87;		
Matches 162;	Conservative 42;	Mismatches 87;	Indels 6;	Gaps 2;

Qy	24	CTFNEKDIVFYVYSPDKRDGILLKKE ^{LT} NYDLFTFKSTYSKQWFLIHGFSLGTNNENFV	833
		: : : : : : : : :	
Db	21	CPFSNDTVKMIFLITRENRKHDFTYLLDTMRNHNEFKSIIKRPFVFITHGFTSSATEKNFV	800

```
Qy      84 AMSKALIEKDPLVISVDWMKKGACNAFASTKDALGYSKAVGNTRHVGEFVADFTKLLEVK 1433
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      81 AMSEALMHTGDFLIMVDWRMAACTDEYPGLYMYFYKAAGVTNRLVGNFIAIATKLVEQ 1400
```

```
QY      144 YKVLISNIRLIGHSLGHTSGFAGKEVOKLKGLKYKEIIGLDPAOPYFHRSDCPDRLCVT 203
        ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      141 YKVPMNTNIRLVGHSLSGAHISGFAGKRVQELKLGFSEIIGLDPAGPSFKNDCSERICET 200
```

```
Qy      204 DAELYVQVHTSIILGVYLYNNGSVDFYANYGKNQPGCN--EPSCSHTKAVKYLTCEIRKE    260
        |||||::||| | :|||:| | ||| | :|||:||||| |||: |
Db      201 DAHYVQLHTSSNLGTERTLGTVDIFYLNNNGSNQPGCRYIIGETCSHTRAVKTYFTECIRRE    260
```

```

Oy      261 CCLIGTPWKKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317
        ||||| :||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db      261 CCLIGVPQSK--NPQPSKCTRNECVCGVNAKKYPKRGSFYVEAEAPYCINNNG 314

```

RESULT 7
US-09-166-205B-17
; Sequence 17, Application US/09166205B

```

: APPLICANT: Te piao KING
: TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES,
: TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL
: TITLE OF INVENTION: THERAPIES BASED THEREON
: FILE REFERENCE: 2313/0F138US
: CURRENT APPLICATION NUMBER: US/09/166,205B
: CURRENT FILING DATE: 1998-10-01
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 17
: LENGTH: 317
: TYPE: PRT
: ORGANISM: Dolichovespula maculata
: US-09-166-205B-17

```

Query Match	50.3%;	Score 866;	DB 3;	Length 317;
Best Local Similarity	54.5%;	Pred. No. 1e-87;		
Matches 162;	Conservative 42;	Mismatches 87;	Indels 6;	Gaps 2;

```

Qy      24 CTFNEKDIVEVYVYSRDKRDGII LKKE TLTYDLFTKSTISKQVVELIHGFLSTGNNEFV 83
      | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      21 CPFSNDTVKMI F LTRNKRKHD FYTLDTMNRHNEFKSII KRPVEITHGFTSSATEKNFV 80

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84 AMSKALIEKDFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGKFVADFTKLVEK 143

```

Db      81  AMSEALMHTGDFLLIMVDWRMAACTDEYFGLKYMFFYKAAGNTRLVGNFIAMIAKLVLEQ 140
QY      144  YKVLISNIRLIGHSLGAHTSGFAGKEVOKLKGKYKEIIGLDPAGPYFHRSDCPDRLCVT 203
Db      141  YKVPMTNIRLVGHSLSGAHISGFAGKRVQELKLGKFSLEIIGLDPAGPSFKKNDCSERICET 200
QY      204  DAEYVQVHTHSIILGVYYNVSVDFFVNYGKNQPGCN--EPSCSHTKAVKYLTECICKHE 260
Db      201  DAHYVQILHTSSNLGTERTLGIVDFYINNGSNQPGCYIIIGETCSHTRAVKYFTECIRRE 260
QY      261  CCLIGTPWKYFYSTPKPISQCRGDTVCVGLNAKSYARGAFYAPVEANAPYCHNEG 317
Db      261  CCLIGVPSK--NPQPVSKCTIRNECVCVGLNAKYPKRGSFYVPVEAEAPYCNNG 314

```

RESULT 8
US-09-806-658-7

```

; Sequence 7, Application US/09806658
; Patent No. 6652851
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF POLISTINAE VENOM ENZYMES, S
; TITLE OF INVENTION: PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BAS
; FILE REFERENCE: 2313/1F138-US1
; CURRENT APPLICATION NUMBER: US/09/806,658
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Dolichovespula maculata
US-09-806-658-7

```

Query Match	50.3%	Score 866;	DB 4;	Length 317;
Best Local Similarity	54.5%	Pred. No. 1e-87;		
Matches 162; Conservative	42;	Mismatches 87;	Indels 6;	Gaps 2;

```

Oy      24 CTFNEKDIVFYVYSRDKRDGIIKKETLTNYDLEFTKSTISKQVFLIHGFLSTGNNEFV 83
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      21 CPE$NDTVKMIPLTRENKRDFTYLTDTMNRHNEPKSIIKRPVFEITHGFTTSATEKNFV 80

```

Oy 84 AMSKALIEKDDELVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGKFVADFTKLVEK 143
|||::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 81 AMSEALMHTGDPELLIMDWRRMACTDEYPGLKMYFYKAAGNTRLVGNFIAIACKLVEQ 140

```
Oy      144 YKVLISNIRLIGSLGAHTSGFAGREVOKLKGKYKEITGLDPAGPYFHRSDCPDRLCVT 203
        ||::|||:|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      141 YKVPMNTNRILVGHSLGAHISGFAGRVOELKLGKFSEITGLDPAGPSFKNDCSERCET 200
```

```

Oy      204 DAHYVQVHTSIILGVYNNVGSVDPIYVNGKNQPGCN--EPSCSHTKAVKYLTECLKHE 260
      |||::||| |::|||:| ||| |::|||:| |||:|
Db      201 DAHYVQILHTSSNLGTERTLGVDFYINNGSNQPGCRYILGELCSHTRAVKYFTECLRRE 260

```

Oy

261 CCLIGTPMKKVFSTPEKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCINNEG 317
| | | : | : | : | : | : | : | : |
| | | : | : | : | : | : | : | : |

Dz

261 CCLIGVPQS---NPQPSVKCTRNECVCGLNAAKKPKRGSFYVPVEAEAPYCINNNG 314
| | | : | : | : | : | : | : | : |

RESULT 9
PCT-US94-02629-17
; Sequence 17, Application PC/TUS9402629

/ APPLICANT: King, Te-piao
 /
 / TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
 /
 / TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
 /
 / TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
 /
 / NUMBER OF SEQUENCES: 62
 /
 / CORRESPONDENCE ADDRESS:
 /
 / ADDRESSEE: Klauber & Jackson
 /
 / STREET: 411 Hackensack Avenue
 /
 / CITY: Hackensack

```
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02629
; FILING DATE: 10-MAR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/180,209
; FILING DATE: 11-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/031,400
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-074 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-02629-17
```

```
Query Match 50.3%; Score 866; DB 5; Length 317;
Best Local Similarity 54.5%; Pred. No. 1e-87;
Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2;
```

```
QY 24 CTENEKDIVFYVSRDKRDGIIKKETLTNYDLFTKSTISKQVFLIHGFLSTGNNEFV 83
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 21 CPFSNDTVKMIFLTRENKHDFTYLTDMNRHNEFKKSIKRPFVFIITHGFTSSATEKNFV 80
QY 84 AMSKALIEKDDFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGKFNADFTKLVER 143
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 81 AMSEALMHTGDFLIIMVDMWMACTDEYDGLKYMFKAVGNTRLVGNFIAMIAKCLVEQ 140
QY 144 YKVLISNIRLIGHSLGAHTSGFAGKEVOKLKGKYKEIIGLDPAGPYFHRSDCPDRLCVT 203
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 141 YKVPMTNIRLVGHSIGAHSIGFAGKRVQELKGFSEIIGLDPAGPSFKNDCSERICET 200
QY 204 DAEYVQVIHTSIILGVYVNVGSVDYVYVNGKNQPGCN--EPSCSHTKAVKYLTECIRKE 260
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 201 DAHYVQIILHTSSNLGTERLTGTVDFYINNSNQPGCRYIIGETCSHTRAVKYFTECIRRE 260
QY 261 CCLIGTPWKYFSTPKPISQCRGDTVCVCGLNKAKSYPARGAFYAPVEANAPYCHNEG 317
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 261 CCLIGVPOSK--NPQVSKCTRNECVCGLNAKKYPKRGSFYVPEAEAPYCINNNG 314
```

```
RESULT 10
US-08-180-209B-27
; Sequence 27, Application US/08180209B
; Patent No. 5593877
; GENERAL INFORMATION:
; APPLICANT: King, Te-piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
; TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED
; TITLE OF INVENTION: THEREON
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
```

```
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/180,209B
; FILING DATE: 11-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/031,400
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-074 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-180-209B-27
```

```
Query Match 49.7%; Score 856; DB 1; Length 300;
Best Local Similarity 53.2%; Pred. No. 1.2e-86;
Matches 159; Conservative 51; Mismatches 83; Indels 6; Gaps 2;
```

```
QY 22 PDCTENEKDIVFYVSRDKRDGIIKKETLTNYDLFTKSTISKQVFLIHGFLSTGNNEFV 81
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 PKCPFSNDTVSIIETRENRRNDLYTLQTNHPEFKKKTITRPVFIITHGFTSSASETN 61
QY 82 FVAMSKALIEKDDFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGKFNADFTKLIV 141
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 FINLAKALVDKDNVYVISIDWQTACTNEAAGLKLYPYPTAARNTRLVGQYIATITQKLV 121
QY 142 EKYKVLISNIRLIGHSLGAHTSGFAGKEVOKLKGKYKEIIGLDPAGPYFHRSDCPDRLC 201
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 KHYKISMANIRLIGHSLGAHASGFAGKKVQELKGYSEIIGLDPARPSFDSNHCERLC 181
QY 202 VTDAEYVQVIHTSIILGVYVNVGSVDYVYVNGKNQPGCN--EPSCSHTKAVKYLTECIRK 258
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 ETDAEYVQIHTSNYLGTETKLTGTVDFYMNNGKNQPGCGRFSEVCSHSRAVIYMAECIK 241
QY 259 HECCLIGTPWKYFSTPKPISQCRGDTVCVCGLNKAKSYPARGAFYAPVEANAPYCHNEG 317
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 HECCLIGIPRSK--SSQPISSCTKQECVCVGLNAKKTYSRGSFYVPVESTVPFCNNKG 297
```

```
RESULT 11
US-08-385-745-27
; Sequence 27, Application US/08385745
; Patent No. 5612209
; GENERAL INFORMATION:
; APPLICANT: King, Te piao
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
; TITLE OF INVENTION: Based Thereon
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
```



```

1 ZIP: 10036-2711
2
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: Floppy disk
5 COMPUTER: IBM PC compatible
6 OPERATING SYSTEM: PC-DOS/MS-DOS
7 SOFTWARE: PatentIn Release #1.0,
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/08/385,745
10
11 FILING DATE:
12 CLASSIFICATION: 435
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US/08/031,400
15 FILING DATE:
16
17 ATTORNEY/AGENT INFORMATION:
18 NAME: Mistrock, S. Leslie
19 REGISTRATION NUMBER: 18,872
20 REFERENCE/DOCKET NUMBER: 3288-020
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: 212 790-9090
23 TELEFAX: 212 869-8864/9741
24 TELEEX: 66141 PENNIE
25 INFORMATION FOR SEQ ID NO: 27:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 300 amino acids
28 TYPE: amino acid
29 TOPOLOGY: linear
30 MOLECULE TYPE: protein
31
32 US-08-385-745-27

```

Query Match	49.7%;	Score 856;	DB 1;	Length 300;
Best Local Similarity	53.2%;	Pred. No. 1.2e-86;		
Matches 159; Conservative	51;	Mismatches 83;	Indels 6;	Gaps 2;

[illegible]

RESULT 12
US-08-485-388-27

```

; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
; TITLE OF INVENTION: Based Thereon
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
;

```

```

1  COMPUTER:  IBM PC compatible
2  OPERATING SYSTEM:  PC-DOS/MS-DOS
3  SOFTWARE:  PatentIn Release #1.0,  Version #1.25
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER:  US/08/485,388
6  FILING DATE:  07-JUN-1995
7  CLASSIFICATION:  435
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER:  08/385,745
10 FILING DATE:  08-FEB-1995
11 CLASSIFICATION:  435
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER:  08/031,400
14 FILING DATE:  11-MAR-1993
15 CLASSIFICATION:  435
16 ATTORNEY/AGENT INFORMATION:
17 NAME:  Jackson Esq.,  David A.
18 REGISTRATION NUMBER:  26,742
19 REFERENCE/DOCKET NUMBER:  600-1-074  FWCA
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE:  201 487-5800
22 TELEFAX:  201 343-1684
23 TELELEX:  133521
24 INFORMATION FOR SEQ ID NO:  27:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH:  300 amino acids
27 TYPE:  amino acid
28 TOPOLOGY:  linear
29 MOLECULE TYPE:  protein
30
31 US-08-485-388-27

```

Query Match	49.7%	Score 856;	DB 3;	Length 300;
Best Local Similarity	53.2%;	Pred. No. 1.2e-86;		
Matches 159;	Conservative 51;	Mismatches 83;	Indels 6;	Gaps 2;

QY	22	PDCTFENEKDIVFYVYSRDKRDGIILKKELTNTYDLFTKSTISKQVFLIHGFLSTGNNEN	81
		: : : : : : : : :	
Db	2	PKCFPNSDPTVSIIEETRENRNRDLVTYLQTLQNHPEFKKITTTPVVFITHGFTSSASETN	61
QY	82	FVAMSKALIEKDEFLVISVDWKGACNAFASTKDALGYSKAVGNTRHVGKFAVADFTKLLV	141
		: : : : : : : : : :	
Db	62	FINLAKALVDKDNMYMVISIDWQCACTNEAAGLKLYLPPTAARNTRLVGQYIATITQKLV	121
QY	142	EKYKVLISNIRLIGHSLGAHTSGFAGKEVOKLKGKYKEIIGLDPAGPYFHRSDCPDRLC	201
		: : : : :	
Db	122	KHYKISMANIRLIGHSLGAHAGSFAGKVKVQELKLGKYSIELGLDPARPSFDSNHCSERLC	181
QY	202	VTDAEYQVYIHITSIIIGVYVNVGSVDIFYVNYGKNQPGCN--EPSCSHTKAVKYLTECIC	258
		: : : :	
Db	182	ETDAEYVOI IHTSNYLGTEKTLGTVDIFYMNNGNKNQPGCGRPFSEVCSHSRAVIYMAECIC	241
QY	259	HECCLIGFPWKKYFTSTPKPISQCRGDTVCVCGLNAKSYFARGAFYAPVEANAPYCHNEG	317
		: : : : : :	
Db	242	HECCLIGIPKSK--SSQPISSCTKQECVCVGLNAKTYTSRGSFYVPVESTIVPFCNNKG	297

RESULT 13
US-08-474-853-27
; Sequence 27, Application US/08474853

```

1 Patent No. 6287559
2
3 GENERAL INFORMATION:
4
5 APPLICANT: King, Te-piao
6
7 TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
8
9 TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
10
11 TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
12
13 NUMBER OF SEQUENCES: 62
14
15 CORRESPONDENCE ADDRESS:
16
17 ADDRESSEE: Klauber & Jackson
18
19 STREET: 411 Hackensack Avenue
20
21 CITY: Hackensack
22
23 STATE: New Jersey
24
25 COUNTRY: USA
26
27 ZIP: 07601
28
29
30

```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,853
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/180,209
; FILING DATE: 11-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/031,400
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Bag., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-074 CIPB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-853-27
```

```
Query Match          49.7%; Score 856; DB 3; Length 300;
Best Local Similarity 53.2%; Pred. No. 1.2e-86;
Matches 159; Conservative 51; Mismatches 83; Indels 6; Gaps 2;

QY      22 PDCTFNEKDIYFYVYSRDKRDGIILKKEITLTNYDLFTKSTISKQVFLIHGFLSTGNNEN 81
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2 PKCPFNSDVTVSIIEETRENRNRDLTYLQFNHPEFKKTTTRPVVFITHGFTSSASETN 61

QY      82 FVAMSKALIEKDDFLVISVDWKKGCNAFASTKDALGYSKAVGNTRHVGKFNADFTKLLV 141
      | : : ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      62 FINLAKALVDKDNMYVISIDWQTACTNEAAGLKLYYPFAARNTRLVGQYIATITQKLV 121

QY      142 EKYKVLISNIRLIGHSLGAHTSGFAGKEVOKLKGKYKEIIGLDPAGPYFHRSDCPDRLC 201
      : || : : ||| ||| ||| ||| ||| ||| ||| ||| ||| : : : |||
Db      122 KHYKISMANIRLIGHSLGAHSGFAGKKVQELKGKYSIIGLDPARPSFDSNHCSERLC 181

QY      202 VTDAEYVQVIHTSIILGVYVNVGSVDYFVNYGKNQPGCN---EPSCSHTKAVKYLTECIK 258
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      182 ETDAEYVQIHTSNYLGTETKLTGYDFYMNNGKNQPGCGRFSEVCSHRAVIYMAECIK 241

QY      259 HECCLIGTPWKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      242 HECCLIGIPKSK--SSQPISSCTKQECVCVGLNAKKTYSRGSFYVPVESTVPCNNKG 297
```

```
RESULT 14
US-09-806-658-8
; Sequence 8, Application US/09806658
; Patent No. 6652851
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF POLISTINAE VENOM ENZYMES, S
; TITLE OF INVENTION: PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BAS
; FILE REFERENCE: 2313/1F138-US1
; CURRENT APPLICATION NUMBER: US/09/806,658
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Vesputa vulgaris
```

```
US-09-806-658-8

Query Match          49.7%; Score 856; DB 4; Length 300;
Best Local Similarity 53.2%; Pred. No. 1.2e-86;
Matches 159; Conservative 51; Mismatches 83; Indels 6; Gaps 2;

QY      22 PDCTFNEKDIYFYVYSRDKRDGIILKKEITLTNYDLFTKSTISKQVFLIHGFLSTGNNEN 81
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2 PKCPFNSDVTVSIIEETRENRNRDLTYLQFNHPEFKKTTTRPVVFITHGFTSSASETN 61

QY      82 FVAMSKALIEKDDFLVISVDWKKGCNAFASTKDALGYSKAVGNTRHVGKFNADFTKLLV 141
      | : : ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      62 FINLAKALVDKDNMYVISIDWQTACTNEAAGLKLYYPFAARNTRLVGQYIATITQKLV 121

QY      142 EKYKVLISNIRLIGHSLGAHTSGFAGKEVOKLKGKYKEIIGLDPAGPYFHRSDCPDRLC 201
      : || : : ||| ||| ||| ||| ||| ||| ||| ||| : : : |||
Db      122 KHYKISMANIRLIGHSLGAHSGFAGKKVQELKGKYSIIGLDPARPSFDSNHCSERLC 181

QY      202 VTDAEYVQVIHTSIILGVYVNVGSVDYFVNYGKNQPGCN---EPSCSHTKAVKYLTECIK 258
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      182 ETDAEYVQIHTSNYLGTETKLTGYDFYMNNGKNQPGCGRFSEVCSHRAVIYMAECIK 241

QY      259 HECCLIGTPWKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      242 HECCLIGIPKSK--SSQPISSCTKQECVCVGLNAKKTYSRGSFYVPVESTVPCNNKG 297
```

```
RESULT 15
PCT-US94-02629-27
; Sequence 27, Application PC/TUS9402629
; GENERAL INFORMATION:
; APPLICANT: King, Te-Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
; TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02629
; FILING DATE: 10-MAR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/180,209
; FILING DATE: 11-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/031,400
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Bag., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-074 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-02629-27
```

Query Match 49.7%; Score 856; DB 5; length 300;
Best local Similarity 53.2%; Pred. No. 1.2e-86;
Matches 159; Conservative 51; Mismatches 83; Indels 6; Gaps 2;

Qy	22	PDCTFNEKDIVFYVYSRDKRDGIIKKETLTNYDLFTKSTISKQVFLIHGFLSTGNEN	81
		: : : : : : : :	
Db	2	PKCFNSDVTVSIIETRENRNDLYTLQTLQNHPEPKKTTITRPVVFITHGFTSSASETN	61
Qy	82	FVAMSKALLIEKODFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGKFAVDFTKLV	141
		: : : : : : : : : : : : :	
Db	62	FINLAKALVDKDNMYMVISIDWQTAACCTNEAAGLKXLYYPTAARNTRLVGQYIATITQKLV	121
Qy	142	EKKYKVLISNIRLIGHSLGAHTSGFAGKEVOKLKGKYEIIGLDPAGPYFHRSDCPDRLC	201
		: : : : : : : : : : : :	
Db	122	KHYKISMANIRLIGHSLGAHSGFAGKVKQELKLGKYSIIIGLDPARPSFDSNHCSERLC	181
Qy	202	VTDAEYVQVIHTSIIIGVYVNVGSDVFYVNYGKNQPGCN--EPSCSHTKAVKYLTECIK	258
		: : : : : : :	
Db	182	ETDAEYVQIHTSNYLGTEKTLGTVDFYMNNGKNQPGCGRFSEVCSHRAVIYMAECIK	241
Qy	259	HECCLIGTPWKKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG	317
		: : : : : : : : : :	
Db	242	HECCLIGIPKSK--SSQPISSCTKQECVCVGLNAKKTYSRGSFYVPVESTVPCNNKG	297

Search completed: April 27, 2005, 12:53:49
Job time : 46 secs

Db	61	TISKQVFLIHGFILSTGNNENFVAMSKALLIEKDDFLVITSVDMKKGACNAFASTKALGYS	120
QY	121	KAVGNTRHVGEKRVADFTKLVEKYKYLISNIRLIGHSLGAHTSGFAGKEVQKLKLGTYKE	180
Db	121	KAVGNTRHVGEKRVADFTKLVEKYKYLISNIRLIGHSLGAHTSGFAGKEVQKLKLGTYKE	180
QY	181	IIGLDPAGPYFHRSDCPDRLCVTDAEYQVIHTSIILGVYINVGSVDFYVNYGKNPGCN	240
Db	181	IIGLDPAGPYFHRSDCPDRLCVTDAEYQVIHTSIILGVYINVGSVDFYVNYGKNPGCN	240
QY	241	EPSCSHTKAVKYLTECIKHCCCLIGTFPWKKYFSTPKPISQCGDTCVCVGLNAKSYPARG	300
Db	241	EPSCSHTKAVKYLTECIKHCCCLIGTFPWKKYFSTPKPISQCGDTCVCVGLNAKSYPARG	300
QY	301	AFYAPVEANADPYCHNEGIXL	320
Db	301	AFYAPVEANADPYCHNEGIXL	320

```

RESULT 2
US-09-847-208-88
; Sequence 88, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847, 208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Dolichovespula maculata (White-face hornet)
US-09-847-208-88

```

Query Match	55.2%;	Score 949.5;	DB 10;	Length 303;
Best Local Similarity	57.6%;	Pred. No. 1e-88;		
Matches 175; Conservative	52;	Mismatches 68;	Indels 9;	Gaps 5;

[illegible]

RESULT 3
US-09-847-208-168
; Sequence 168, Application US/09847208
; Publication No. US20030082190A1

```

; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 168
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Vespula vulgaris (Yellow jacket) (Wasp)
US-09-847-208-168

Query Match          50.8%; Score 873.5; DB 10; Length 336;
Best Local Similarity 52.0%; Pred. No. 7.6e-81;
Matches 166; Conservative 55; Mismatches 87; Indels 11; Gaps 4;

```

[illegible]

```

RESULT 4
US-09-847-208-87
; Sequence 87, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847, 208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
;
; LENGTH: 317
;
; TYPE: PRT
;
; ORGANISM: Dolichovespula maculata (white-face hornet)
US-09-847-208-87

```

Query Match	50.3%;	Score 866;	DB 10;	Length 317;
Best Local Similarity	54.5%;	Pred. No. 4.1e-80;		
Matches 162;	Conservative 42;	Mismatches 87;	Indels 6;	Gaps 2;
QY	24	CTFNEKDIVFVYVSRDKRDGIIILKETTITNYDLFTKSTISKQVFLIHGFLSTGNNEFV	83	
	:	:	:	:


```
Db      21 CPFSNDTVKMIFLTRENKHDFTYLTDMNRHNEFKKSIKRPFVFTTHGFTSSATEKNFV 80
;
QY      84 AMSKALIEKDEFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGFVADFTKLLVEK 143
;
Db      81 AMSEALMHTGDFLIIMVDMRMAACTDEYEPGLKMYFYKAAVGNTRLVGNFIAMIAKKLV EQ 140
;
QY      144 YKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYEIIGLDPAGPYFHRSDCPDRLCVT 203
;
Db      141 YKVPMTNIRLVGHSLSGAHISGFAGKRVQELKGKFESEIIGLDPAGPSFKKNDCSERICET 200
;
QY      204 DAEYVQVHTSIILGVYVNVGSVDYFVYVNGKNQPGCN--EPSCSHTKAVKYLTECIRKE 260
;
Db      201 DAHYVQIHTSSNLGTERLTGTVDFYINNGSNQPGCRYIIGETCSHTRAVKYFTECIRRE 260
;
QY      261 CCLIGTPWKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317
;
Db      261 CCLIGVPOSK--NPQVSKCTRNECVCVGLNAKKYPRKGRSFYVPEAEAPYCNNG 314
```

```
RESULT 5
US-10-688-011-7
; Sequence 7, Application US/10688011
; Publication No. US20040175393A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF POLISTINAE VENOM ENZYMES,
; TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL
; FILE REFERENCE: 02313/100F138-US2
; CURRENT APPLICATION NUMBER: US/10/688,011
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 09/806,658
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US99/23211
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 09/166,205
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Dolichovespula maculata
US-10-688-011-7
```

```
Query Match      50.3%; Score 866; DB 16; Length 317;
Best Local Similarity 54.5%; Pred. No. 4.1e-80;
Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2;

QY      24 CTFNEKDIVFYVS RDKRDGIILKKELTNYDLFTKSTISKQOVFLIHGFLSTGNNEFV 83
;
Db      21 CPFSNDTVKMIFLTRENKHDFTYLTDMNRHNEFKKSIKRPFVFTTHGFTSSATEKNFV 80
;
QY      84 AMSKALIEKDEFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGFVADFTKLLVEK 143
;
Db      81 AMSEALMHTGDFLIIMVDMRMAACTDEYEPGLKMYFYKAAVGNTRLVGNFIAMIAKKLV EQ 140
;
QY      144 YKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYEIIGLDPAGPYFHRSDCPDRLCVT 203
;
Db      141 YKVPMTNIRLVGHSLSGAHISGFAGKRVQELKGKFESEIIGLDPAGPSFKKNDCSERICET 200
;
QY      204 DAEYVQVHTSIILGVYVNVGSVDYFVYVNGKNQPGCN--EPSCSHTKAVKYLTECIRKE 260
;
Db      201 DAHYVQIHTSSNLGTERLTGTVDFYINNGSNQPGCRYIIGETCSHTRAVKYFTECIRRE 260
;
QY      261 CCLIGTPWKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317
;
Db      261 CCLIGVPOSK--NPQVSKCTRNECVCVGLNAKKYPRKGRSFYVPEAEAPYCNNG 314
```

```
RESULT 6
US-09-847-208-164
; Sequence 164, Application US/09847208
```

```
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Vespula maculifrons (Eastern yellow jacket) (Wasp)
US-09-847-208-164
```

```
Query Match      50.2%; Score 864; DB 10; Length 300;
Best Local Similarity 54.0%; Pred. No. 6.1e-80;
Matches 162; Conservative 51; Mismatches 79; Indels 8; Gaps 4;

QY      22 PDCTNEKDIVFYVS RDKRDGIILKKELTNYDLFTKSTISKQOVFLIHGFLSTGNNEFV 81
;
Db      2 PKCFNSDVTISIETRENKRDLYTLQTLQNHPEFKKTTTRPVFTTHGFTSSASEKN 61
;
QY      82 FVAMSALIEKDEFLVISVDWKKGAC-NAFASTKDALGYSKAVGNTRHVGFVADFTKLL 140
;
Db      62 FINLAKALVDKDNVVISIDWQTACTNEYPLKAY-YPTAASNTRLVGVIATITQKL 120
;
QY      141 VEKYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYEIIGLDPAGPYFHRSDCPDRL 200
;
Db      121 VKDYKSMANIRLIGHSLGAHVS GFAGKRVQELKGKFESEIIGLDPARPSFDSNHCSERL 180
;
QY      201 CVTDAEVQVHTSIILGVYVNVGSVDYFVYVNGKNQPGCN--EPSCSHTKAVKYLTECI 257
;
Db      181 CETDAEVQIHTSNYLGTEKILGTVDFYMNNGKNNPGCGRPFSEVCSHTRAVIYMAECI 240
;
QY      258 KHECCLIGTPWKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317
;
Db      241 KHECCLIGIPRSK--SSQPIRSCTKQECVCGVLAKKYPRSGSFYVPEASTAPFCNNKG 297
```

```
RESULT 7
US-10-688-011-8
; Sequence 8, Application US/10688011
; Publication No. US20040175393A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF POLISTINAE VENOM ENZYMES,
; TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL
; FILE REFERENCE: 02313/100F138-US2
; CURRENT APPLICATION NUMBER: US/10/688,011
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 09/806,658
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US99/23211
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 09/166,205
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-688-011-8
```

```
Query Match      49.7%; Score 856; DB 16; Length 300;
Best Local Similarity 53.2%; Pred. No. 4.1e-79;
Matches 159; Conservative 51; Mismatches 83; Indels 6; Gaps 2;
```

```
QY 22 PDCTFNEKDIVEFVYSRDKRDGIIILKKELTNTYDLFTKSTISKOVFLIHGFLSTGNEN 81
Db 2 PKCFNSDVTWSIIETRENRNRDLTYTLQTNHPEFKKTTITRPVVFITHGFTSSASETN 61
QY 82 FVAMSKALIEKDFLVISVDWKGCANAFSTKDALGSKAVGNTRHVKGFEVADFTKLV 141
Db 62 FINLAKALVDKDNMYVISIDWQTAACITNEAAGLKVLYPTAARNTLVGOYIATITQKLV 121
QY 142 EKYKVLISNIRLIGHSLGAHTSGFAGKEVQKLGKYKEIIGLDPAGPYFHRSDCPDRLC 201
Db 122 KHYKISMANIRLIGHSLGAHAGSFGAKKQVQLGKYSEIIGLDPARPSFDSNHCSERLC 181
QY 202 VTDAEYQVIHTSIILGVYVNGSVDFYVNYGKNQPGCN--EPSCSHTKAVKYLTECIC 258
Db 182 ETDAEYQVIHTSNYLGTTEKTGLTVDFYMNNGKNQPGCGRFFSEVCSHSRAVIYMAECIC 241
QY 259 HECCLIPTWKKYFSTPKPIISQCRGDTCCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317
Db 242 HECCLIPTPKSK--SSQPIISCTKQECVCVGLNAKSYTSGSFYVPVESTVFPCCNNKG 297
```

RESULT 8

```
US-10-467-248-5
; Sequence 5, Application US/10467248
; Publication No. US20040086905A1
; GENERAL INFORMATION:
; APPLICANT: DAS, Debopriya; YAO, Monique G.;
; APPLICANT: ARVIZU, Chandra S.; BAUGHN, Mariah R.;
; APPLICANT: LU, Yan; HAFALIA, April J.A.;
; APPLICANT: CHAWLA, Nandinder K.; GRIFFIN, Jennifer A.;
; APPLICANT: LU, Dyoung Aina M.; YUE, Henry;
; APPLICANT: FORSTHE, Ian J.; RAMKUMAR, Jayalaxmi;
; APPLICANT: GANDHI, Ameena R.; ISON, Craig H.;
; APPLICANT: WARREN, Bridget A.; TANG, Y. Tom;
; APPLICANT: EMERLING, Brooke M.; HONCHELL, Cynthia D.;
; APPLICANT: LYNE, Michael; BARROSO, Ines
; TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES
; FILE REFERENCE: PI-0358 USN
; CURRENT APPLICATION NUMBER: US/10/467,248
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03813
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,910
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/276,891
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/276,855
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/279,760
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/283,818
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/285,405
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474074CD1
US-10-467-248-5
```

```
Query Match 19.7%; Score 339; DB 15; Length 415;
Best Local Similarity 32.8%; Pred. No. 8.3e-26;
Matches 96; Conservative 38; Mismatches 107; Indels 52; Gaps 11;
QY 53 NYDLFTKSTISKQVFLIHGFLSTGN---NENFVAMSKALIEKDFLVISVDWKGCACN 108
Db 18 NNSLNVNFTQKKTWVLHGYRPVGSIPLWLQNFV---RILLNEEDMNVIVVDSRGATTT 74
```

```
QY 109 AFASTKDALGYSKAVGNTRHVGVADFTKLVVEKYKVLISNIRLIGHSLGAHTSGFAGK 168
Db 75 FI-----YNRAVKNTRKVAVSLSVHIKNLL-KHGASLDNFHFIFGSLGAHISGFVG- 124
QY 169 EVQKLGKGYKEIIGLDPAGPYFHRSDCPDRLCVTDAEYQVIHT-SIILGVYVNGSV 227
Db 125 ---KIFHGQLGRITGLDPAGPRFSRKPYPYSLDYTDAKFVDVIHSDSNGLGIOEPLGHID 181
QY 228 FYVNYGKNQPGCNEP-----SCSHTKAVKYLTECIKHECCLIPTWKKY--FSTPKP 277
Db 182 FYPNGGNKQPGCPKSIIFSIGIQFIKCNHQRAVHLFMAASLETNCNFIISFPCRSYKDYKT--- 238
QY 278 ISQC-----RGDTCCVGLNAKSY-----PARGAFYAPVEANAPYC 313
Db 239 -SLCVDCCDFKEKSCPRLGQAQLFKGVLEKRMGRPLRTTVFLDTSGTYPPFC 290
```

RESULT 9

```
US-09-963-160-12
; Sequence 12, Application US/09963160
; Publication No. US20030165845A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Chung, Miyoung
; TITLE OF INVENTION: 47647, A No. US20030165845A1e1 Human Lipase and Uses Therefor
; FILE REFERENCE: 10147-48U1
; CURRENT APPLICATION NUMBER: US/09/963,160
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/234,915
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-963-160-12
```

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Query Match 19.7%; Score 339; DB 10; Length 489;
Best Local Similarity 32.8%; Pred. No. 1e-25;
Matches 96; Conservative 38; Mismatches 107; Indels 52; Gaps 11;
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QY 53 NYDLFTKSTISKQVFLIHGFLSTGN---NENFVAMSKALIEKDFLVISVDWKGCACN 108
Db 92 NNSLNVNFTQKKTWVLHGYRPVGSIPLWLQNFV---RILLNEEDMNVIVVDSRGATTT 148
QY 109 AFASTKDALGYSKAVGNTRHVGFVADFTKLVVEKYKVLISNIRLIGHSLGAHTSGFAGK 168
Db 149 FI-----YNRAVKNTRKVAVSLSVHIKNLL-KHGASLDNFHFIFGSLGAHISGFVG- 198
QY 169 EVQKLGKGYKEIIGLDPAGPYFHRSDCPDRLCVTDAEYQVIHT-SIILGVYVNGSV 227
Db 199 ---KIFHGQLGRITGLDPAGPRFSRKPYPYSLDYTDAKFVDVIHSDSNGLGIOEPLGHID 255
QY 228 FYVNYGKNQPGCNEP-----SCSHTKAVKYLTECIKHECCLIPTWKKY--FSTPKP 277
Db 256 FYPNGGNKQPGCPKSIIFSIGIQFIKCNHQRAVHLFMAASLETNCNFIISFPCRSYKDYKT--- 312
QY 278 ISQC-----RGDTCCVGLNAKSY-----PARGAFYAPVEANAPYC 313
Db 313 -SLCVDCCDFKEKSCPRLGQAQLFKGVLEKRMGRPLRTTVFLDTSGTYPPFC 364
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RESULT 10

```
US-10-872-198-41
; Sequence 41, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPT
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOETSMEIER
```

```

; APPLICANT: Ulrich Ketting
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.0002U4
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 434
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: chimera of guinea pig and homo sapiens (human= approx. last 30 aa
; US-10-872-198-41

```

	Query Match	19.5%	Score 336;	DB 16;	Length 434;	
	Best Local Similarity	32.9%;	Pred. No. 1.8e-25;			
	Matches	91;	Conservative	39;	Mismatches 111;	Indels 36; Gaps 8;
Qy	44 IILKETLTNYDLFTKSTI-----SKOVFLIHGFIISTGNNEFVAMSKALIEKD	93				
Dd	40 LLYTNNQNNSYQLITATDIATIKASNFNLNRKTRFIHGFSDSGENSWLSDMCKNMFCQE	99				
Qy	94 DFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGKFVADFTKLIVKKYLISNRL	153				
Dd	100 KVNCCICVDWKGGS-----KAQYSQASQINRVRGAEVAYLVQVLSTSLNYPAPENVHI	150				
Qy	154 IGHSIGAHTSGFAGKEVOKLKGKYKEIIGLDPAGPYFHRSDCPD--RLCVTDAEYYOVI	211				
Dd	151 IGHSIGAHTAGEAGKRNL----GLVGRITGLDPAEPFY--QDTPEEVRLLPSPDAKFVDVI	204				
Qy	212 HT-----SIILGVYVNVGSVDIFYVNYGKNQPGCNEP--SCSHTKAVKYLITECIKHCCCL	263				
Dd	205 HTDISPIPLPSLGFGMSQYGVHMDFFPNGGKOMPGCKTGISCNHHRHSIEYHSSILNPEGF	264				
Qy	264 ICTPWKKYFSTPKP-ISQCRGDDTCVCVGLNAKSYPAR	299				
Dd	265 LGYPCASYDEFQESGCPCCPAKGCCPKMGHFADQYPGK	301				

RESULT 11
US-10-872-197A-41
; Sequence 41, Application US/10872197A
; Publication No. US20050059126A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOTSMEIER
; APPLICANT: Ulrich KETTLING
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.000203
; CURRENT APPLICATION NUMBER: US/10/872,197A
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-11-10

```

; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 434
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: chimera of guinea pig and homo sapiens (human= approx. last 30
; US-10-872-197A-41

```

	Query Match	19.5%;	Score 336;	DB 17;	length 434;	
	Best Local Similarity	32.9%;	Pred. No. 1.8e-25;			
	Matches	91;	Conservative	39;	Mismatches 111;	Indels 36; Gaps 8
Qy	44 IILKKEITLNYDLFTKSTI-----SKÖVFLIHGFLSTGNNEFVAMSKALLIEKD	93				
Db	40 LLYTNNQNSYQLITATDIATIKASNFNLNRKTRFIHGFTDSENSWLSDMCKMFEQE	99				
Qy	94 DFLVISVDWKKGACNAFASTKDALGYSAVGNTRHVGFEVADFTKLVEKKYKVLISNIRL	153				
Db	100 KVNCICTDWKGG-----KAQYSQASQNI RRVGAEVAYLVLQVLSTSLNVAENVHI	150				
Qy	154 IGHSIGAHTSGFAGKEVQKLKGKYKEIIGLDPAGPYEHRSDCPD--RLCVTPDAEYVQVI	211				
Db	151 IGHSLGAHTAGEAGKRIN----GLVGRITGLDPAEPYF--QDTPEEVRLDPSDAKFVDVI	204				
Qy	212 HT-----SIILGVYYNVGSVDFFVNYGKNQPGCNEP--SCSHTKAVKYLTECTIHECC	263				
Db	205 HTDISPIILPSLGFGMSQKVGHMDFFPNNGCKDMFGCKTGISCNHRSIEYHSSILNPEGF	264				
Qy	264 IGTPMKKYFSTPKP-ISQCRBDTCVCVGLNAKSYPAR	299				
Db	265 LGYPCASYDEFOESGCFCPPCAKGCPRMGHFADQYPGK	301				

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RESULT 12
US-10-163-547-5
; Sequence 5, Application US/10163547
; Publication No. US20030037350A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Myers, Rachel
; APPLICANT: Rudolf-Owen, Laura A.
; TITLE OF INVENTION: No. US20030037350A1el nucleic acid sequences encoding a
; TITLE OF INVENTION: human ubiquitin protease, lipase, dynamin, short chain
; TITLE OF INVENTION: dehydrogenase, and ADAM-TS Metalloprotease and uses
; TITLE OF INVENTION: therefore
; FILE REFERENCE: 35800/247836(5800-243)
; CURRENT APPLICATION NUMBER: US/10/163,547
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 09/407,356
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/704,918
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 09/435,311
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 09/796,100
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,503
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 09/781,598
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/182,009
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/782,952
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,408
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/496,005
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 22

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RESULT 15
US-10-220-380-5
; Sequence 5, Application US/10220380
; Publication No. US20030113846A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: YAO, Monique G.
; APPLICANT: YUE, Henry
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TANG, Y. Tom
; APPLICANT: KHAN, Farrah A.
; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: DAS, Debopriya
; APPLICANT: HILMAN, Jennifer L.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: HAFALIA, April
; APPLICANT: TRIBOULEY, Catherine M.
; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
; FILE REFERENCE: PI-0050 PCT
; CURRENT APPLICATION NUMBER: US/10/220,380
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/186,480; 60/190,415; 60/198,437
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030113846A1 5027764CD1
US-10-220-380-5

Query Match      18.7%; Score 322; DB 14; Length 451;
Best local Similarity 30.8%; Pred. No. 5.2e-24;
Matches 92; Conservative 51; Mismatches 112; Indels 44; Gaps 13;

QY      44 IILKKEITLT-----NYDLFTKSTISKQVFLIHGFLSTGNNENFV-AMSKALIEKDFLV 97
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      44 MLYTRKNLTCAQTINSSAFGNLNVTKTTFIVHGFRPTGSPVWMDLVKGLSVEDMNV 103

QY      98 ISVDWKKGACNAFASTKDALGYSKAVGNTRHVGKFAVF- TKLLVEKYKVLISNIRLIGH 156
      :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      104 VVVDWNRGA-----TTLIYTHASSKTRKVMVLMKEFIDQMLAE--GASLDDIYMGV 153

QY      157 SLGAHTSGFAGKEVQKLKGKYKEITIGLDPAGPYFHRSDCPDRLCVTDAEYVQVHTSI- 215
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      154 SLGAHISGFVG-EMYDGLGR---ITGLDPAGPLFNGKPHQDRLDPSDAQFVDVHSDTD 209

QY      216 ILGVYVNGSVDFVNVYGNQPGCNEP-----SCSHTKAVKYLTECIKHECCCLIGTP 267
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      210 ALGYKEPLGNIDFPYNGGLDQPGCPKTIILGGFQYFKCDHQRSVYLYLSSLRESCITTAYP 269

QY      268 WKY--FSTPKPIS--QCRGDTVCVVG-----LNKSYPARGAFYAPVEANAPYC 313
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      270 CDSYQDYRNGKCVSCGTSQKESCPILGYADNMKDHRLRGKDPMTKAFEDTAE-ESPPFC 327
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Search completed: April 27, 2005, 13:06:04
Job time : 138 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2005, 12:44:47 ; Search time 40 Seconds
(without alignments)
769.734 Million cell updates/sec

Title: US-10-688-011-2

Perfect score: 1721

Sequence: 1 ICFLLDSTFRNGTLNRGM.....AFYAPVEANAPYCHNEGIKL 320

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	949.5	55.2	303	2	A44563	phospholipase A1 (
2	866	50.3	317	2	S32406	phospholipase A1 -
3	864	50.2	300	2	A44564	triacylglycerol A1 (
4	336	19.5	434	1	A49488	triacylglycerol 1i
5	321	18.7	449	1	LIPG	triacylglycerol 1i
6	312.5	18.2	461	2	S21223	triacylglycerol 1i
7	309	18.0	465	2	C43357	lipoprotein lipase
8	307.5	17.9	474	1	A40570	lipoprotein lipase
9	307.5	17.9	474	1	JH0790	lipoprotein lipase
10	306.5	17.8	470	2	A54232	lipase, CoPL-RP2 -
11	305.5	17.8	475	1	LIHUL	lipoprotein lipase
12	305.5	17.8	475	2	JC4242	lipoprotein lipase
13	304.5	17.7	450	1	A27053	lipoprotein lipase
14	304.5	17.7	478	2	S29846	lipoprotein lipase
15	302.5	17.6	465	1	A27330	lipoprotein lipase
16	297.5	17.3	467	2	A43357	pancreatic lipase
17	297.5	17.3	478	2	S18158	lipoprotein lipase
18	296	17.2	482	1	A46696	triacylglycerol 1i
19	293.5	17.1	469	2	B43357	pancreatic lipase
20	292.5	17.0	457	2	I48206	triacylglycerol 1i
21	292	17.0	490	1	S04331	lipoprotein lipase
22	290.5	16.9	482	1	A34671	triacylglycerol 1i
23	289.5	16.8	465	2	S41084	triacylglycerol 1i
24	288.5	16.8	473	2	S20612	triacylglycerol 1i
25	287.5	16.7	467	1	LIPG	triacylglycerol 1i
26	279	16.2	499	2	A28997	triacylglycerol 1i
27	273.5	15.9	465	1	JC1318	triacylglycerol 1i
28	268	15.6	510	2	S15893	triacylglycerol 1i
29	257	14.9	494	2	A27442	triacylglycerol 1i

30	167	9.7	439	1	VJFF1	vitellogenin I pre
31	154	8.9	437	2	S22889	vitellogenin 1 - M
32	153	8.9	356	2	S49011	yolk protein 2 - b
33	134.5	7.8	420	2	A25876	vitellogenin III p
34	129	7.5	422	2	S49012	yolk protein 3 - b
35	128	7.4	442	1	VJFF2	vitellogenin II pr
36	125.5	7.3	172	2	A45658	triacylglycerol 1i
37	124	7.2	422	2	S22888	vitellogenin 2 - M
38	102	5.9	851	2	A59284	unconventional myo
39	100.5	5.8	601	2	T34396	hypothetical prote
40	100	5.8	540	2	G96716	hypothetical prote
41	98	5.7	400	2	S46814	ribosomal protein
42	97.5	5.7	494	2	T05302	vacuolar processin
43	96.5	5.6	261	2	S69709	hypothetical prote
44	96.5	5.6	909	2	T33749	hypothetical prote
45	96	5.6	261	1	F70390	probable phosphoes

ALIGNMENTS

RESULT 1

A44563

phospholipase A1 (EC 3.1.1.32), allergen Dol m 1.02 - bald-faced hornet

C/Species: Vesputula maculata (bald-faced hornet)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C/Accession: A44563

R/Hoffman, D.R.

submitted to the Protein Sequence Database, February 1994

A/Reference number: A44563

A/Accession: A44563

A/Molecule type: protein

A/Residues: 1-303 <HOF>

A/Cross-references: UNIPROT:P53357

A/Note: 55-Glu was also found; 295-Tyr was also found

C/Superfamily: triacylglycerol lipase

C/Keywords: carboxylic ester hydrolase

Query Match

Best local Similarity 55.2%; Score 949.5; DB 2; Length 303;
Best local Similarity 57.6%; Pred. No. 1.2e-69;
Matches 175; Conservative 52; Mismatches 68; Indels 9; Gaps 5;

QY	19	GMSPDCTFNEKDIVFYYSRDKRDGIILKKEITLNYDLFTKSTI-SKQVFLIHGFLSTG	77
DB	1	GILPECKLVPEEISFVLSTFENRDGVYLLTQKLNKGMFKNSDLSKKVFLIHGFISSA	60
QY	78	NNENFVAMSKALIEKDDFVIVSDWKKGAC-NAPASTKDALGYSKAVGNTRHVGKFAVADF	136
DB	61	TNKNYVADMTRALDQKDIWIVISIDWRDGAACSNFALLK-FIGYPKAVENTRAVGKIADF	119
QY	137	TKLVEKCYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKKEITGLBPAGPYFHRSDC	196
DB	120	SKLIQKCYKVLLENIRLIGHSLGAQIAGFAGKEFQRFKLGKYPEITIGLDAGPSFKKDC	179
QY	197	PDRLCVTDABEVQVVIHTSIILGVYVNVGSVDFFVYVNGKQPGCN---EPCSHTKAVKYL	253
DB	180	PERICETDAHYVQIILHTSNLGTERTLGTVDFTINDGSNPGCTYIIGETCSHTRAVKYL	239
QY	254	TECIRHBCCLIGTPWKYFTSTPKPISQCRGDTCCVGLNAKSYPARGAFYAPVEANAPYC	313
DB	240	TECIRRECCILIGVPSK---NPQVPSKCTRNBCVGLNAKEYPKKGSFYVVEAKAPFC	296
QY	314	HNEG 317	
DB	297	NNNG 300	

RESULT 2

S32406

phospholipase A1 - bald-faced hornet (fragment)

C/Species: Vesputula maculata (bald-faced hornet)

C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C/Accession: S32406

R.Soldatova, L.; Kochoumian, L.; King, T.P.

FEBS Lett. 320, 145-149, 1993

A:Title: Sequence similarity of a hornet (D. maculata) venom allergen phospholipase A(1)

A:Reference number: S32406; MUID:93209375; PMID:8458431

A:Accession: S32406

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-317 <SOL>

A:Cross-references: UNIPROT:Q06478; EMBL:X66869; NID:g288916; PID:g288917

C:Superfamily: triacylglycerol lipase

Query Match 50.3%; Score 866; DB 2; Length 317;

Best Local Similarity 54.5%; Pred. No. 8e-63;

Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2;

QY 24 CTFNEKDIVFVYSRDKRDGIIKKETLTNYDLFTKSTISKQVFLIHGFLSTGNNEFV 83

Db 21 CFFSNDTVKMIFLTRENKHDFTYLTDMNRHNEFKSIIKRPVFIHGFTHGFTSSATEKNFV 80

QY 84 AMSKALIEKDDFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGKFAVDFTKLLVEK 143

Db 81 AMSKALMHGTDFLIIMVDWMAACTDEYPLKYMFKAAVGNTRLVGNFLAMIAKLVQ 140

QY 144 YKVLISNIRLIGHSLGAHTSGPAGKEVQKLKGKYEIIIGLDPAGPYFHSDCPDRLCVT 203

Db 141 YKVPMTNIRLVGHSLSGAHTSGPAGKRVQELKGFSEIIIGLDPAGPSFKKNDCSERICET 200

QY 204 DAEYQVQIHTSIILGVYVNGSVDFYVNYGKNQPGCN--EPSCSHTKAVKYLTECIKHE 260

Db 201 DAHYVQILHTSSNLGTERLTGTVDFYINNGSNQPGCRYIIGETCSHTRAVKYFTECIRRE 260

QY 261 CCLIGTPWKKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317

Db 261 CCLIGVPOSK--NPQPVSKCTRNECVCGLNAAKYPKRGSFYVPVEAEPYCNNG 314

RESULT 3

A44564

phospholipase A1 (EC 3.1.1.32), allergen Ves m 1 - eastern yellowjacket

C:Species: Vesputia maculifrons (eastern yellowjacket)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C:Accession: A44564

R.Hoffman, D.R.

submitted to the Protein Sequence Database, February 1994

A:Reference number: A44563

A:Accession: A44564

A:Molecule type: protein

A:Residues: 1-300 <HOF>

A:Cross-references: UNIPROT:P51528

A:Note: 97-Met was also found; 191-Pro was also found; 202-Leu was also found

C:Superfamily: triacylglycerol lipase

C:Keywords: carboxylic ester hydrolase

Query Match 50.2%; Score 864; DB 2; Length 300;

Best Local Similarity 54.0%; Pred. No. 1.1e-62;

Matches 162; Conservative 51; Mismatches 79; Indels 8; Gaps 4;

QY 22 PDCTFNEKDIVFVYVSRDKRDGIIKKETLTNYDLFTKSTISKQVFLIHGFLSTGNNEFV 81

Db 2 PKCFNSDVTVSIIEITRENRRDLTYLTQIQNHPFKKKTITRPVFIHGFTHGFTSSASEKN 61

QY 82 FVAMSKALIEKDDFLVISVDWKKGAC-NAFASTKDALGYSKAVGNTRHVGKFAVDFTKLL 140

Db 62 FVNLAKALVDKDNMNVISIDWQTACTNEYPGLKAY-YPTAASNTRLVGQYIATITQKL 120

QY 141 VEKYKVLISNIRLIGHSLGAHTSGPAGKEVQKLKGKYEIIIGLDPAGPYFHRSDCPDRL 200

Db 121 VQYKISMNIRLIGHSLGAHTSGPAGKRVQELKGFSEIIIGLDPAPPSFDSNHCSERL 180

QY 201 CVTDAEVQVQIHTSIILGVYVNGSVDFYVNYGKNQPGCN--EPSCSHTKAVKYLTECI 257

Db 181 CETDAEVQIHTSNYLGTETKILGTVDFYMNNGKNNPGCGRFSEVCSHTRAVIYMAECI 240

QY 258 KHECCLTGTPWKKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317

Db 241 KHECCLTGIPRSK---SSQPISRCTKQECVCVGLNAKYPSPRGSFYVPESTAPFCNNKG 297

RESULT 4

A49488

triacylglycerol lipase (EC 3.1.1.3), pancreatic - guinea pig

C:Species: Cavia porcellus (guinea pig)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A49488

R.Hjorth, A.; Carriere, F.; Cudrey, C.; Woldike, H.; Boel, E.; Lawson, D.M.; Ferrato, F

Biochemistry 32, 4702-4707, 1993

A:Title: A structural domain (the lid) found in pancreatic lipases is absent in the guin

A:Reference number: A49488; MUID:93257433; PMID:8490016

A:Accession: A49488

A:Status: preliminary; translation not shown; not compared with conceptual translation

A:Molecule type: mRNA; protein

A:Residues: 1-434 <HJO>

A:Cross-references: UNIPROT:P81139

A:Experimental source: pancreas

A:Note: sequence extracted from NCBI backbone (NCBIP:132521)

C:Superfamily: triacylglycerol lipase

C:Keywords: carboxylic ester hydrolase

F,154,178,247/Active site: Ser, Asp, His #status predicted

Query Match 19.5%; Score 336; DB 1; Length 434;

Best Local Similarity 32.9%; Pred. No. 1.3e-19;

Matches 91; Conservative 39; Mismatches 111; Indels 36; Gaps 8;

QY 44 IILKETLTNYDLFTKSTI-----SKQVFLIHGFLSTGNNEFVAMSKALIEKD 93

Db 40 LLYTNNQNSYQLITATDIATIKASNFNLNRKTRFIHGFTHGFTDSENSWLSDMCKMFOVE 99

QY 94 DFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGKFAVDFTKLLVEKYKVLISNIRL 153

Db 100 KVNCTICVDWKGS-----KAQYQASQNIIRVGAEVAYLVQLSTSLNYPAPENVHI 150

QY 154 IGHSLGAHTSGPAGKEVQKLKGKYEIIIGLDPAGPYFHRSDCPD--RLCVTDAEVQVI 211

Db 151 IGHSLGAHTAGGAKRLN---GLVGRITGLDPAEPYF--QDTPEVRILDPDAKFAVDVI 204

QY 212 HT-----SIILGVYVNGSVDFYVNYGKNQPGCNEP-SCSHTKAVKYLTECIKHECCL 263

Db 205 HTDISPLPSLGFQMSQKVGHMDFFPNGCKDMPGCKTGISCNHRSIEYHSSILNPEGF 264

QY 264 IGTPWKKYFSTPKP-ISQCRGDTVCVGLNAKSYPAR 299

Db 265 LGYPCASYDEFQESGCFPCPAKGCPRKMGHRADQYPGK 301

RESULT 5

LIPG

triacylglycerol lipase (EC 3.1.1.3) - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 30-Nov-1980 #sequence_revision 22-May-1981 #text_change 31-Mar-2000

C:Accession: A90638; A91256; A90675; A91124; A00732

R.De Caro, J.; Boudouard, M.; Bonicel, J.; Guidoni, A.; Desnuelle, P.; Rovey, M.

Biochim. Biophys. Acta 671, 129-138, 1981

A:Title: Porcine pancreatic lipase. Completion of the primary structure.

A:Reference number: A90638; MUID:82113655; PMID:7326260

A:Accession: A90638

A:Molecule type: protein

A:Residues: 308-449 <DEC>

A:Experimental source: pancreas

R.Bianchetto, J.D.; Bidaud, J.; Guidoni, A.A.; Bonicel, J.J.; Rovey, M.

Eur. J. Biochem. 97, 395-405, 1979

A:Title: Porcine pancreatic lipase. Sequence of the first 234 amino acids of the peptide

A:Reference number: A91256; MUID:79236335; PMID:380992

A:Contents: carbohydrate-binding site

A:Accession: A91256

A:Molecule type: protein

A:Residues: 1-234 <BIA>

A;Experimental source: pancreas
R;Guidont, A.; Bonicel, J.; Blanchetta, J.; Rovey, M.
Biochimie 61, 841-845, 1979
A;Title: Porcine pancreatic lipase. Sequence between the 235th and 307th amino acids.
A;Reference number: A90675; MUID:80088446; PMID:518929
A;Accession: A90675
A;Molecule type: protein
A;Residues: 235-307 <GUI>
A;Experimental source: pancreas
A;Note: this sequence has since been revised at positions 302 and 305
R;Benkouka, F.; Guidont, A.A.; De Caro, J.D.; Bonicel, J.J.; Desnuelle, P.A.; Rovey, M.
Eur. J. Biochem. 128, 331-341, 1982
A;Title: Porcine pancreatic lipase. The disulfide bridges and the sulfhydryl groups.
A;Reference number: A91124; MUID:83105095; PMID:7151781
A;Contents: disulfide bonds
A;Accession: A91124
A;Molecule type: protein
A;Residues: 1-182,'E',184-449 <BEN>
A;Experimental source: pancreas
R;Guidont, A.; Benkouka, F.; De Caro, J.; Rovey, M.
Biochim. Biophys. Acta 660, 148-150, 1981
A;Title: Characterization of the serine reacting with diethyl p-nitrophenyl phosphate in
A;Reference number: A90634; MUID:82000578; PMID:6791692
A;Contents: annotation; substrate-binding site
C;Comment: Ser-152 reacts with emulsified or micellar diethyl p-nitrophenyl phosphate and
C;Superfamily: triacylglycerol lipase
C;Keywords: carboxylic ester hydrolase; glycoprotein; lipid digestion
F;4-10,237-261,285-296,299-304,433-449/Disulfide bonds: #status experimental
F;90-101/Disulfide bonds: (or 90-103) #status experimental
F;166/Binding site:carbohydrate (Asn) (covalent) #status experimental

Query Match	18.7%	Score 321;	DB 1;	Length 449;
Best Local Similarity	28.4%	Pred. No. 2.3e-18;		
Matches	88;	Conservative	50;	Mismatches 122;
			Indels	50;
			Gaps	8;

[illegible]

```

RESULT 6
S21223
triacylglycerol lipase (EC 3.1.1.3) precursor, pancreatic - horse (fragment)
C/Species: Equus caballus (domestic horse)
C/Date: 22-Nov-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: S21223; S21251
R/Kerfeltec, B.; Foglizzo, E.; Bonicel, J.; Bougis, P.E.; Chapus, C.
Eur. J. Biochem. 206, 279-287, 1992
A/Title: Sequence of horse pancreatic lipase as determined by protein and cDNA sequencing
A/Reference number: S21223; MUID:92267022; PMID:1587279
A/Accession: S21223
A/Molecule type: mRNA
A/Residues: 1-461 <KER>

```

A;Cross-references: UNIPROT:P29183; EMBL:X66218; NID:g1063; PIDN:CAA46961.1; PID:g1064
A;Accession: S21251
A;Molecule type: protein
A;Residues: 13-78;80;97-218;220-228;230-277;322-349;384-438;440-448;450-461 <KEW>
C;Superfamily: triacylglycerol lipase
C;Keywords: carboxylic ester hydrolase
F;1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F;13-461/Product: triacylglycerol lipase #status experimental <MAT>

Query Match	18.2%;	Score 312.5;	DB 2;	Length 461;
Best Local Similarity	29.0%;	Pred. No. 1.1e-17;		
Matches	86;	Conservative 41;	Mismatches 123;	Indels 47;
				Gaps 7;

```

QY      33 FVYVSRRDKRDG---IILKKETLTNYDLFTYKSTIISKÖVFLIHGFLSTGNNENFVAMSKAL 89
      | : : : | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      51 FLTYTNNPNDFNOEIVADPSTIQSSNENT---GRKTRFIIHGFIDKEEBSWLTWCQNM 106
      | : : : | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      90 IEKDFLVIISVDMKKGACNAFASTKDALGYSKAVGNTRHVGFVADFTKLVEKKYVLIS 149
      : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      107 FKVESVNCICVDMWKSGRTA-----YSQASQNVRI GA EVA YLVGLVQSSFDYSPS 157
      | : : : | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      150 NIRLIGHSLGAHTSGFAGKEVQKLKGKYKEIIGLDPAGPYFHRSDCPRLCTVDAEYVQ 209
      | : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      158 NVHIIHGLSHAGAEAGRRTN---GAVGRITGLDPAEPFCQTPELVRLDPSDAQFVD 213
      | : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      210 VIHTSII-----LGVYYNVGSVDFYVNYGKNQPGCNE-----PS 243
      | | | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      214 VIHTDIAPFIENLGFMSQTAGHLDFPNCGKEMPGCQKXVLSQIVDIDGITWQTRDFAA 273
      | : : : | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      244 CSHTKAVKYLTECIKHECCLLIGTPWKKYFS-TPKPISQCRGDTVCVCGLNAKSYPAR 299
      | : : : | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      274 CNHLRSYKYITDSILNPDGFAGFSCASYSDFTANKCFPCSSEGC PQMGHYADRFPGR 330

```

RESULT 7

C43357

triacylglycerol lipase (EC 3.1.1.3) precursor, pancreatic - human

N;Alternate names: fatty acid ethyl ester synthase; pancreatic lipase

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: C43357; A34494; S08272; A60135; S34578; A34574

R;Giller, T.; Buchwald, P.; Blum-Kaelin, D.; Hunziker, W.

J. Biol. Chem. 267, 16509-16516, 1992

A;Title: Two novel human pancreatic lipase related proteins, hPLRP1 and hPLRP2. Differ

A;Reference number: A43357; MUID:92355622; PMID:1379598

A;Accession: C43357

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 1-465 <GIL>

A;Cross-references: UNIPROT:P16233; GB:M33285; NID:g190139; PIDN:AAA60129.1; PID:g190140

R;Lowe, M.E.; Rosenblum, J.L.; Strauss, A.W.

J. Biol. Chem. 264, 20042-20048, 1989

A;Title: Cloning and characterization of human pancreatic lipase cDNA.

A;Reference number: A34494; MUID:90062115; PMID:2479644

A;Accession: A34494

A;Molecule type: mRNA

A;Residues: 1-465 <LOW>

A;Cross-references: GB:J05125; NID:g339596; PIDN:AAA36740.1; PID:g339597

R;Winkler, F.K.; D'Arcy, A.; Hunziker, W.

Nature 343, 771-774, 1990

A;Title: Structure of human pancreatic lipase.

A;Reference number: S08272; MUID:90158821; PMID:2106079

A;Accession: S08272

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 17-46;48-465 <WIN>

A;Note: part of this sequence, including the amino end of the mature protein, was confir

R;de Caro, A.; Bonicel, J.; Pleroni, G.; Guy, O.

Biochimie 63, 799-801, 1981

A;Title: Comparative studies of human and porcine pancreatic lipases: N-terminal sequen

A;Reference number: A60135; MUID:82069208; PMID:7306587

A;Accession: A60135

A;Molecule type: protein

A:Residues: 17-30, 'X', 32-33, 'X', 35-36, 'IOX', 40-41, 'X', 43-45 <DEC>
R:Thirstrup, K.; Carriere, F.; Hjorth, S.; Rasmussen, P.B.; Woeldike, H.; Nielsen, P.F.;
FEBS Lett. 327, 79-84, 1993
A:Title: One-step purification and characterization of human pancreatic lipase expressed
A:Reference number: S34578; MUID:93327921; PMID:8335100
A:Accession: S34578
A:Status: preliminary
A:Molecule type: protein
A:Residues: 17-31 <THI>
R:Riley, D.J.S.; Kyger, E.M.; Spilburg, C.A.; Lange, L.G.
Biochemistry 29, 3848-3852, 1990
A:Title: Pancreatic cholesterol esterases. Purification and characterization of human pa
A:Reference number: A34574; MUID:90283377; PMID:2354155
A:Accession: A34574
A:Molecule type: protein
A:Residues: 'X', 18-36 <RIL>
A:Experimental source: pancreas
C:Genetics:
A:Gene: GDB:PNLIP
A:Cross-references: GDB:127916; OMIM:246600
A:Map position: 10q24-10q26
C:Superfamily: triacylglycerol lipase
C:Keywords: carboxylic ester hydrolase
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-465/Product: triacylglycerol lipase #status experimental <MAT>

Query Match	18.0%;	Score 309;	DB 2;	Length 465;
Best Local Similarity	30.7%;	Pred. No. 2.2e-17;		
Matches 92;	Conservative 40;	Mismatches 106;	Indels 62;	Gaps 9;

OY	48 KETLTNYDLFT-----KSTIS-----KÖVELIHGFLSTGNNEPVA-MS	86
Dd	49 KDVNTREFLTYNENPNNFÖEVAADSSISGSNFKTRKTRFIHGFIDKG-EENWLANVC	107
OY	87 KALIEKDDELVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGVFADFTKLVEKKYV	146
Dd	108 KNLFKEVESVNCICVDWKGGS-----RTGYTQASÖNIRIVGAEVAYFEFLQSAGY	158
OY	147 LISNRILGHSLGAHTSGFAGKEVÖKULGKYKEIIGLDPAEPYFHRSDCPDRLCVTDAAE	206
Dd	159 SPSNVHVIHGSLGAHAAGEAGRRTN----GTIGRITGLDPAEPCFGTPELVRLDPSDAK	214
OY	207 YVÖVIHT-----SIILGVYYNVSVDFFVNYGKNÖPGCNE-----	241
Dd	215 FVDVIHTDGAPIVPNLGFGMSÖVGHLDFFPNNGGVEMPGCKAKNILSÖIVIDIDIGIWEGTRD	274
OY	242 -PSCSHTKAVKYLTECIKHCCCLIGTPWKKY-FSTPKPIISOGRGDTCVCVGMLAKSYPAR	299
Dd	275 FAACNHLSRYKYTTDSIVNPDDGFAGFPFCASYNVFTANKCPFCPSGGCOPMGHYADRYPGK	334

RESULT 8
A40570
lipoprotein lipase (EC 3.1.1.34) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A40570, JH0513; A60948; A29300; I55526
R:Zechner, R.; Newman, T.C.; Steiner, E.; Breslow, J.L.
Genomics 11, 62-76, 1991
A:Title: The structure of the mouse lipoprotein lipase gene: a BI repetitive element is
A:Reference number: A40570; MUID:92112227; PMID:1765386
A:Accession: A40570
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-474 <ZEC>
A:Cross-references: UNIPROT:P1152; GB:M60846
R:Hua, X.; Enerback, S.; Hudson, J.; Youkhana, K.; Gimble, J.M.
Gene 107, 247-258, 1991
A:Title: Cloning and characterization of the promoter of the murine lipoprotein lipase-e
A:Reference number: JH0513; MUID:92084117; PMID:1748295
A:Accession: JH0513
A:Status: translation not shown
A:Molecule type: DNA

A/Residues: 1-29 <HUA>
A/Cross-references: GB:M6335; NID:g198830; PIDN:AAC04464.1; PID:g2911254
J.Semenkovich, C.F.; Chen, S.H.; Wims, M.; Luo, C.C.; Li, W.H.; Chan, L.
A/Lipid Res. 30, 423-431, 1989
A/Title: Lipoprotein lipase and hepatic lipase mRNA tissue specific expression, developm
A/Reference number: A60948; MUID:89257126; PMID:2723548
A/Accession: A60948
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A/Molecule type: mRNA
A/Residues: 1-128, 'Y', 130-146, 'N', 148-474 <SEM>
R.Kirchgesner, T.G.; Svenson, K.L.; Lusis, A.J.; Schotz, M.C.
J. Biol. Chem. 262, 8463-8466, 1987
A/Title: The sequence of cDNA encoding lipoprotein lipase. A member of a lipase gene fam
A/Reference number: A29300; MUID:87250454; PMID:3597382
A/Accession: A29300
A/Molecule type: mRNA
A/Residues: 9-146, 'N', 148-474 <KIR>
A/Cross-references: GB:J03302; GB:J02740; NID:g198849; PIDN:AAA39440.1; PID:g387406
R.Gimble, J.M.; Hua, X.; Youkhana, K.; Bass, H.W.; Medina, K.; Sullivan, M.; Greenberger
J. Cell. Biochem. 50, 73-82, 1992
A/Title: Apidogenesis in a myeloid supporting bone marrow stromal cell line.
A/Reference number: I55526; MUID:93054974; PMID:1339460
A/Accession: I55526
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-146, 'N', 148-184 <RES>
A/Cross-references: GB:M65258; NID:g198863; PIDN:AAA39442.1; PID:g198864
A/Comment: This enzyme is responsible for the hydrolysis of triglycerides into free fatt
C/Superfamily: triacylglycerol lipase
C/Keywords: carboxylic ester hydrolase; glycoprotein
F/1-27/Domain: signal sequence #status predicted <SIG>
F/28-474/Product: lipoprotein lipase #status predicted <MAT>
F/159,183,268/Active site: Ser, Asp, His #status predicted

Query Match	17.9%;	Score 307.5;	DB 1;	Length 474;
Best Local Similarity	31.0%;	Pred. No. 3e-17;		
Matches	88;	Conservative	35;	Mismatches 110;
				Indels 51;
				Gaps 9;

OY	63 SKOVFLIHGFLSTGNENNENFVANSKALIEK--DDELVIISVDWKKGACNAFASTXDALGYS	120
Db	72 SSKTEFVVIIHGWTVTGTMYESWVPKLVAALYKREPDSNVIIVDWLYRAQQHHYPV---SAGYT	128
OY	121 KAVGNTRHVGVKFVADFTKLVEKKYLISNIRLIGHSLGAHTSGFAGEVOQKILGYKE	180
Db	129 KLVGND-----VARFINMWEEBCKPLDNVHLHGYSIGAHAAGVAGSLTNK-----KVNR	178
OY	181 IIGLDPAOPYEHRSDCPRLCTDAEYVQVIHT-----SILGVYYNVGSVDFYVNYGK	234
Db	179 ITGLDPAGENFEYAABSRLSPPDADFVDVLHTFTRGSPGRSIGIQKPVGHVDIYPNGGT	238
OY	235 NQPGCN-----EPSCSHTKAVKYLTCEIKHECCLIGHTPMKKYESTPK	276
Db	239 FQPGCNIGEAIRVIAERGLGDVDOLVKCSHERSIHLFIDSLNE----ENPSKAYRCONS	294
OY	277 PISO-----CRGDTVCVCGELNAKSYPAR--GAFYAPVEANAPY	312
Db	295 BAFEKGLCLICRKXRCNNLGYEINKVRAKRSSKMULTRSQMPY	338

RESULT 9
JH0790
lipoprotein lipase (EC 3.1.1.34) precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: JH0790; A36127
R/Brault, D.; Noe, L.; Etienne, J.; Hamelin, J.; Raisonnier, A.; Souli, A.; Chuat, J.C.,
Gene 121, 237-246, 1992
A/Title: Sequence of rat lipoprotein lipase-encoding cDNA.
A/Reference number: JH0790; MUID:93077037; PMID:1339374
A/Accession: JH0790
A/Molecule type: mRNA
A/Residues: 1-474 <BRA>
A/Cross-references: UNIPROT:Q06000; GB:103294; NID:q205214; PIDN:AAA41534.1; PID:q205215

A;Experimental source: testicular fat cell
A;Note: the authors translated the codon GCC for residue 384 as Ser, AAC for residue 411
R;Raynolds, M.V.; Awald, P.D.; Gordon, D.F.; Gutierrez-Hartmann, A.; Rule, D.C.; Wood, W.
Mol. Endocrinol. 4, 1416-1422, 1990
A;Title: Lipoprotein lipase gene expression in rat adipocytes is regulated by isoproterenol
A;Reference number: A36127, MUID:91042645, PMID:2233752
A;Accession: A36127
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'V', 337-474 <RAY>
C;Superfamily: triacylglycerol lipase
C;Keywords: carboxylic ester hydrolase; glycoprotein; lipid metabolism; plasma
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-474/Product: lipoprotein lipase #status predicted <MAT>
F;159,183,268/Active site: Ser, Asp, His #status predicted

Query Match	17.9%;	Score 307.5;	DB 1;	Length 474;
Best Local Similarity	31.3%;	Pred. No. 3e-17;		
Matches	89;	Conservative 33;	Mismatches 11;	Indels 51; Gaps 9;
Qy	63	SKQVFLIHGFLSTGNNEFVAMSKALIEK--DDFLVISVDMKKGACNAFASTKDALGYS	120	
Db	72	SSKTFVVIHGWTVTGMYESWPKLVAAALYKREPDNSNVIIVDMLYRAQOHYPV--SAGYT	128	
Qy	121	KAVGNTRHVKGKVFADFTKLVEKRYKVLISNIRLIGHSLGHTSGFAGEVQKLKGKYKE	180	
Db	129	KLVGND-----VARFINWEEEFNYPPLDNVHLGLGYSLGAAHAGVAGSLTNK----KVNR	178	
Qy	181	IIGLDPAGPYFHRSDCPRLCTDAEYVQVIHT-----SIIIGVYVNVGSDVFYVNYGK	234	
Db	179	ITGLDPAGPNFEYEAAPSRLSPPDDADFVDVLHTFTRGSPGRSIGIQKPGVHVDIYPNGGT	238	
Qy	235	NQPGCN-----EPSCSHTKAVKYLTECLIKHECCLIIGTPMKKYFSTPK	276	
Db	239	FQPGCNIGEAIRVIAEKGCLGDVDQLVKCSHERSIHLFTIDSLINE-----ENPSKAYRCNSK	294	
Qy	277	PISQ-----CRGDTVCVCGLNAKSYPAR--GAFYAPVEANADPY	312	
Db	295	EAFEGKGLCSCKRNRCNNVGYEINKVRAKRSSKMYYLKTROOMPYP	338	

RESULT 10
A54232
lipase, CoPL-RP2 - nutria
C/Species: Myocastor coypus (nutria, coypu)
C/Date: 22-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A54232
R/Thirstrup, K.; Verger, R.; Carriere, F.
Biochemistry 33, 2748-2756, 1994
A/Title: Evidence for a pancreatic lipase subfamily with new kinetic properties.
A/Reference number: A54232; MUID:94176463; PMID:8130186
A/Accession: A54232
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-470 <THI>
A/Cross-references: UNIPROT:Q64424
A/Experimental source: pancreas
A/Note: sequence extracted from NCBI backbone (NCBIP:144530)
C/Superfamily: triacylglycerol lipase

```

Query Match      17.8%; Score 306.5; DB 2; Length 470;
Best Local Similarity 28.2%; Pred. No. 3.6e-17;
Matches 93; Conservative 49; Mismatches 115; Indels 73; Gaps 12;

QY      14 GTLNRM-----SPDCTFNEKDIVFYVYSRDKRDGIIKKETLTNYDLFTKS----- 60
      ||| | : || : : | : | || | :
Db      37 GTLQRPVKS LPA S P E - S I N T R - - - F L L Y T - - - - - N E N P N N Y Q I L I T A T D P A T I K A S 82

QY      61 --TISKQVFLIHGFLSTGNNE NFVAMSKALIEKQDPLVSYDWMKKGACNAFASTKDALG 118
      : : : | : | : | : | : | : | : | : | : | :
Db      83 NFNLHRTKRFVIHGFIDNGEKDWLTDICRMFOVEKVNCCIVDWQGGSLAI----- 133

QY      119 YSKAVGNTRHVGKFEVADFTYLLVEKYKVLISNRLIGHSLGAHTSGFAGKEVQKLKLGKY 178

```

Db 134 YSQAQVQNRVVGAEVAYLVQVLSQDLGYKPGNVHMIGHSLGAHTAAEAGRRLK----GLV 189

QY 179 KEIIGLDPAQPFYFHRSDCPD--RLCVTDAEYVQVIHTSI-----LGVYYNNGSVDFY 229

Db 190 GRITGLDEAEPFCF--QDTPEEVRLDPSDAMFVDVIHTDIAPIIPSFGFGMSQKVGHMDF 247

QY 230 VNYGKNQPGCNE-----PSCSHTKAVKYLTECIKHECCLGTPWKK 270

Db 248 PNGGKEMPGCEKNIISTIVDVNGFLEGITSLAACNHMRSIQYSSSILNPDGFLGYPCAS 307

QY 271 YFSTPKP-ISQCRGDTVCVGLNAKSYPAR 299

Db 308 YEFPQKDGCFPPCAEGCCKPMGHYADQFOGK 337

RESULT 11

LIHL

lipoprotein lipase (EC 3.1.1.34) precursor - human

N/Alternate names: LPL

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1987 #sequence revision 30-Sep-1987 #text change 09-Jul-2004

C/Accession: A26082; S03710; S13552; PH0849; A42050; B42050; C42050; A39044; S10575; I3

R/Wion, K.L.; Kirchgessner, T.G.; Lusis, A.J.; Scholtz, M.C.; Lawn, R.M.

Science 235, 1638-1641, 1987

A/Title: Human lipoprotein lipase complementary DNA sequence.

A/Reference number: A26082; MUID:87149101; PMID:3823907

A/Accession: A26082

A/Molecule type: mRNA

A/Residues: 1-475 <WIO>

A/Cross-references: UNIPROT:P06858; GB:M15856; NID:g187209; PIDN:AAB59536.1; PID:g30713

R/Gotoda, T.; Senda, M.; Gamou, T.; Furuichi, Y.; Oka, K.

Nucleic Acids Res. 17, 2351, 1989

A/Title: Nucleotide sequence of human cDNA coding for a lipoprotein lipase (LPL) cloned

A/Reference number: S03710; MUID:89202044; PMID:2701938

A/Accession: S03710

A/Molecule type: mRNA

A/Residues: 1-475 <GOT>

A/Cross-references: EMBL:X14390; NID:g34404; PIDN:CAA32564.1; PID:g34405

R/Takagi, A.; Ikeda, Y.; Yamamoto, A.

Nucleic Acids Res. 18, 6436, 1990

A/Title: DNA sequence of lipoprotein lipase cDNA cloned from human monocytic leukemia T

A/Reference number: S13552; MUID:91057142; PMID:2243796

A/Accession: S13552

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 1-475 <TAKI>

A/Cross-references: EMBL:X54516; NID:g34382; PIDN:CAA38372.1; PID:g34383

R/Chuat, J.C.; Ratsonnier, A.; Etienne, J.; Galibert, F.

Gene 110, 257-261, 1992

A/Title: The lipoprotein lipase-encoding human gene: sequence from intron-6 to intron-9

A/Reference number: PH0849; MUID:92165069; PMID:1537564

A/Accession: PH0849

A/Molecule type: DNA

A/Residues: 341-475 <CHU>

A/Cross-references: GB:M76722; NID:g187215; PIDN:AAA59528.1; PID:g553523

R/Ma, Y.H.; Brulin, T.; Tuzgöl, S.; Wilson, B.I.; Roederer, G.; Liu, M.S.; Davignon, J.;

J. Biol. Chem. 267, 1918-1923, 1992

A/Title: Two naturally occurring mutations at the first and second bases of codon aspar-

6 is essential for catalysis.

A/Reference number: A42050; MUID:92112922; PMID:1730727

A/Accession: A42050

A/Molecule type: DNA

A/Residues: 182,'G',184-186 <MA1>

A/Cross-references: GB:S76125; NID:g242985; PIDN:AAB20998.1; PID:g242986

A/Note: sequence extracted from NCBI backbone (NCBIN:76125, NCBI:P:76132)

A/Accession: B42050

A/Molecule type: DNA

A/Residues: 239-242,'S',244-247 <MA2>

A/Cross-references: GB:S76077; NID:g242987; PIDN:AAB20999.1; PID:g242988

A/Note: sequence extracted from NCBI backbone (NCBIN:76077, NCBI:P:76131)

A/Accession: C42050

A/Molecule type: DNA

A;Residues: 182,'N',184-189 <MA3>
A;Cross-references: GB:S76076; NID:g242989; PIDN:AAB21000.1; PID:g242990
A;Note: sequence extracted from NCBI backbone (NCBIN:76076, NCBI:P:76129)
A;Note: these mutations were identified in patients with LDL deficiency
R;Dichek, H.L.; Fojo, S.S.; Beg, O.U.; Skarlatos, S.I.; Brunzell, J.D.; Cutler Jr., G.B.
J. Biol. Chem. 266, 473-477, 1991
A;Title: Identification of two separate allelic mutations in the lipoprotein lipase gene
A;Reference number: A39044; MUID:91093167; PMID:1702428
A;Accession: A39044
A;Molecule type: mRNA
A;Residues: 219-223;268-272 <DIC>
A;Note: normal sequence is shown; alleles with mutations of 221-Ile to Thr or of 270-Arg
R;Oka, K.; Tkalecivic, G.T.; Nakano, T.; Tucker, H.; Ishimura-Oka, K.; Brown, W.V.
Biochim. Biophys. Acta 1049, 21-26, 1990
A;Title: Structure and polymorphic map of human lipoprotein lipase gene.
A;Reference number: S10575; MUID:90291024; PMID:1972631
A;Accession: S10575
A;Molecule type: DNA
A;Residues: 1-5;26-34;79-88;139,'D',141-148;177-185;255-263;336-344;376-384;437-445;472-
A;Cross-references: GB:X52978; GB:X53518; NID:g34386
A;Note: this translation is not annotated in GenBank entry HSLIPASE, release 114.0
R;Enerback, S.; Ohlsson, B.G.; Samuelsson, L.; Bjursell, G.
Mol. Cell. Biol. 12, 4622-4633, 1992
A;Title: Characterization of the human lipoprotein lipase (LPL) promoter: evidence of tw
PL gene during adipogenesis.
A;Reference number: I37996; MUID:93024407; PMID:1406652
A;Accession: I37996
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-5 <ENE>
A;Cross-references: EMBL:X68111; NID:g34389; PIDN:CAA48230.1; PID:g4379028
R;Gotoda, T.; Yamada, N.; Kawamura, M.; Kozaki, K.; Mori, N.; Ishibashi, S.; Shimano, H.
J. Clin. Invest. 88, 1856-1864, 1991
A;Title: Heterogeneous mutations in the human lipoprotein lipase gene in patients with F
A;Reference number: I55564; MUID:92091492; PMID:1752947
A;Accession: I55564
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 228-230,'E',232-233 <GOT1>
A;Cross-references: GB:S71706; NID:g240930; PIDN:AAB20664.1; PID:g240931
A;Accession: I70232
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 268-269,'H',271-273 <GOT2>
A;Cross-references: GB:S71710; NID:g240928; PIDN:AAB20663.1; PID:g240929
R;Takagi, A.; Ikeda, Y.; Tsutsumi, Z.; Shoji, T.; Yamamoto, A.
J. Clin. Invest. 89, 581-591, 1992
A;Title: Molecular studies on primary lipoprotein lipase (LPL) deficiency. One base dele
A;Reference number: I55573; MUID:92147877; PMID:1737848
A;Accession: I55573
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 246-247,'LSA', <TAK2>
A;Cross-references: GB:S81339; NID:g245360; PIDN:AAB21420.1; PID:g245361
A;Note: mutant sequence from patients with primary lipoprotein lipase deficiency
C;Comment: The primary function of this lipase is the hydrolysis of triglycerides of ch
protein C-II on the luminal surface of vascular endothelium, where it is anchored by a m
C;Genetics:
A;Gene: GDB:LPL, LIPD
A;Cross-references: GDB:120700; OMIM:238600
A;Map position: 8p22-8p22
A;Introns: 380/2; 441/2
C;Complex: homodimer
C;Function:
A;Description: catalyzes the hydrolysis of triacylglycerol to diacylglycerol plus a fatt
A;Pathway: lipid degradation
C;Superfamily: triacylglycerol lipase
C;Keywords: carboxylic ester hydrolase, glycoprotein; lipid degradation; plasma
F;1-27/Domains: signal sequence #status predicted <SIG>
F;28-475/Product: lipoprotein lipase #status predicted <MPT>
F;152-169/Region: lipid binding #status predicted
F;54-67,243-266,291-310,302-305,445-465/Disulfide bonds: #status predicted
F;70,386/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

F,159,183,268/Active site: Ser, Asp, His #status predicted

Query Match      17.8%; Score 305.5; DB 1; Length 475;
Best Local Similarity 30.3%; Pred. No. 4.4e-17;
Matches 86; Conservative 36; Mismatches 111; Indels 51; Gaps 8;

QY      63 SKQVFLIHGFLLSTGNNENFVAMSKALIEK--DDFLVISVDWKKGACNAFASTKDALGYS 120
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      72 SSKTFMVIHGWITVTGMYESWPKLVAAALYKREPDNSNVIIVDWLSRAQE-----HYF 122

QY      121 KAVGNTIRHVGKFNADFTKLVEKYYKVLISNRLLIGHSLGAHTSGFAGKEVOKLKGKYKE 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      123 VSAGYTKLVGDVARFINMMEEFNPLDNVHLLGYSLGAAHAGIAGSLTNK---KVNK 178

QY      181 IIGLDPAQPYFHRSDCPDRLCVTDAEYVOYIHT-----SIILGVYINVGSDVFYVNYGK 234
      | | | | | | | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      179 ITGLDPAGPNFEYAEAPSRSLSPDDADFDVYLHTFTTRGSPGRSIGIQKPVGHVDIYPNGGT 238

QY      235 NQPGCN-----EPSCSHTKAVKYLTECIKHECCLIIGTPWKKYFSTPK 276
      | | | | | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      239 FQPGCNIGEAIRVIAERGLGDVDQLVKCSHERSIHLFIDSLINE---ENPSKAYRCSSK 294

QY      277 PISQ-----CRGDTVCVGLNAKSYPAR--GAFYAPVEANAPY 312
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      295 BAFEKGLCLSCRNRCNNLGYEINKVRAKRSSKMYLKTRSQMPY 338

```

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RESULT 12
JC4242
lipoprotein lipase (EC 3.1.1.34) precursor - baboon
C/Species: Papio sp. (baboon)
C/Date: 12-Oct-1995 #sequence_revision 08-Feb-1996 #text_change 18-Jun-1999
C/Accession: JC4242
R/Cole, S.A.; Hixson, J.E.
Gene 161, 265-269, 1995
A/Title: Baboon lipoprotein lipase: cDNA sequence and variable tissue-specific expressio
A/Reference number: JC4242; MUID:95394368; PMID:7665091
A/Accession: JC4242
A/Molecule type: mRNA
A/Residues: 1-475 <COL>
A/Cross-references: GB:U18091; NID:g602295; PIDN:AAC50199.1; PID:g602296
C/Comment: This enzyme plays a fundamental role in lipid metabolism by catalyzing the hy
C/Genetics:
A/Gene: lpl
C/Superfamily: triacylglycerol lipase
C/Keywords: carboxylic ester hydrolase; glycoprotein; lipoprotein
F/1-27/Domain: signal sequence #status predicted <SIG>
F/28-475/Product: lipoprotein lipase #status predicted <MAT>
F/70,386/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/159,183,268/Active site: Ser, Asp, His #status predicted

Query Match          17.8%; Score 305.5; DB 2; Length 475;
Best Local Similarity 30.3%; Pred. No. 4.4e-17;
Matches 86; Conservative 36; Mismatches 111; Indels 51; Gaps 8;

QY 63 SKQVFLIHGFLSTGNNENFVAMSKALIEK--DDFLVISVDWKKGACNAFASTKDALGYS 120
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 72 SSKTFMVTIHGWTVTGMYESWPKLVALYKREPSNVIVDWLSRA-----QQHYP 122

QY 121 KAVGNTRHVGEKFEVADFTKLIVKYYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKE 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 123 VSAGYTKLVGQDVARFINMMEEFNYPLDNVHLGLGSAHAAGIAGSLTNK----KVNK 178

QY 181 IIGLDPAQPYFHRSDCPDRLCVTDAEYVQVIHT-----SIILGVYVNVGSVDIFYVNYGK 234
   | | | | | | | | : : | | | : : : : : : : : : : : : : : :
DB 179 ITGLDPAGNFEYAEAPRSLSPDDADFVDVLTHTFTRGSPGRSIGIQKPEGVHVDIYPNGGT 238

QY 235 NQPGCN-----EPGCSHTKAVKYLTECIKHCECLIGTPWKKYFSTPK 276
   ||||| : : : : : : : : : : : : : : : : : : : : : :
DB 239 FQPGCNIGEAIRVIAERGLGDVDQLVKCSHERSIHLFIDSLNE-----ENPSKAYRCSSK 294

QY 277 PISQ-----CRGDTVCVGLNAKSYPAR--GAFYAPVEANAPY 312
   : | : | : | : | : | : | : | : | : | : | : | : |

```

Db 295 EAFKGLCLSCRKNRCNNLGYEINKVRAKRSSKMYLKTQRSQMPY 338

RESULT 13

A27053

lipoprotein lipase (EC 3.1.1.34) - bovine
C/Species: Bos primigenius taurus (cattle)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000

C/Accession: A27053; A34407; A26501

R/Senda, M.; Oka, K.; Brown, W.V.; Qasba, P.K.; Furuchi, Y.

Proc. Natl. Acad. Sci. U.S.A. 84, 4369-4373, 1987

A/Title: Molecular cloning and sequence of a cDNA coding for bovine lipoprotein lipase.

A/Reference number: A27053; MUID:87260809; PMID:2885834

A/Accession: A27053

A/Molecule type: mRNA

A/Residues: 1-450 <SEN>

A/Cross-references: GB:M16966; NID:g163304; PIDN:AAA30624.1; PID:g163305

R/Yang, C.Y.; Gu, Z.W.; Yang, H.X.; Rohde, M.F.; Gotto Jr., A.M.; Pownall, H.J.

J. Biol. Chem. 264, 16822-16827, 1989

A/Title: Structure of bovine milk lipoprotein lipase.

A/Reference number: A34407; MUID:89380314; PMID:2674142

A/Accession: A34407

A/Molecule type: protein

A/Residues: 1-215,'F',217-450 <YAN>

R/Bengtsson-Olivecrona, G.; Olivecrona, T.; Jornvall, H.

Eur. J. Biochem. 161, 281-288, 1986

A/Title: lipoprotein lipases from cow, guinea-pig and man. Structural characterization

A/Reference number: A91178; MUID:87054027; PMID:3536511

A/Accession: A26501

A/Molecule type: protein

C/Superfamily: triacylglycerol lipase

C/Keywords: carboxylic ester hydrolase; glycoprotein

F;29-42,218-241,266-285,277-280,420-440/Disulfide bonds: #status experimental

F;45,361/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;134,158,243/Active site: Ser, Asp, His #status predicted

Query Match 17.7%; Score 304.5; DB 1; Length 450;

Best Local Similarity 30.3%; Pred. No. 5e-17;

Matches 86; Conservative 35; Mismatches 112; Indels 51; Gaps 8;

QY 63 SKQVFLIHGFLSTGNNEFVAMSKALIEK--DDFLVISVDWKKGACNAFASTKDALGYS 120

Db 47 SSKTFVVIHGWTVTGMYESWPKLVAAALYKREPDNSNVIVDWLSRA-----QOHYP 97

QY 121 KAVGNTRHVGKFPVADFTKLVEKRYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKE 180

Db 98 VSAGYTKLVGQDVAKFMMWMADEFNYPPLGNVHLLGYSLGAHAAGIAGSLTNK----KVN 153

QY 181 IIGLDPAGPYFHRSDCPDRLCVTDAYVQVIHT-----SIILGVYNNVGSVDIFYVNYGK 234

Db 154 ITGLDPAGPNFEYAEAPSRSLSPDDADFVDVLTFTRGSPGRSIGIQKPVGHVDIYPNGGT 213

QY 235 NQPGCN-----EPSCSHTKAVKYLTECIKHECCLIGTPMKYFSTPK 276

Db 214 FQPGCNIGELALRVIAERGLGDVDQLVKCSHERSVHLFIDSLNE---ENPSKAYRCNSK 269

QY 277 PISQ-----CRGDTVCVGLNAKSYPAR--GAFYAPVEANAPY 312

Db 270 EAFKGLCLSCRKNRCNNMGYEINKVRAKRSSKMYLKTQRSQMPY 313

RESULT 14

S29846

lipoprotein lipase (EC 3.1.1.34) precursor - sheep

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 08-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C/Accession: S29846; S25615

R/Edwards, W.D.; Daniels, S.E.; Page, R.A.; Volpe, C.P.; Kille, P.; Sweeney, G.E.; Cryer

Biochim. Biophys. Acta 1172, 167-170, 1993

A/Title: Cloning and sequencing of a full length cDNA encoding ovine lipoprotein lipase.

A/Reference number: S29846; MUID:93176802; PMID:8439555

A/Accession: S29846

A/Molecule type: mRNA

A/Residues: 1-478 <EDM>

A/Cross-references: UNIPROT:Q29524; EMBL:X68308; NID:g1812; PIDN:CAA48384.1; PID:g1813

A/Note: the authors translated the codon ACA for residue 391 as Ser

C/Superfamily: triacylglycerol lipase

C/Keywords: carboxylic ester hydrolase; glycoprotein

Query Match 17.7%; Score 304.5; DB 2; Length 478;

Best Local Similarity 30.3%; Pred. No. 5.3e-17;

Matches 86; Conservative 35; Mismatches 112; Indels 51; Gaps 8;

QY 63 SKQVFLIHGFLSTGNNEFVAMSKALIEK--DDFLVISVDWKKGACNAFASTKDALGYS 120

Db 75 SSKTFVVIHGWTVTGMYESWPKLVAAALYKREPDNSNVIVDWLSRA-----QOHYP 125

QY 121 KAVGNTRHVGKFPVADFTKLVEKRYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKE 180

Db 126 VSAGYTKLVGQDVAKFMMWMADEFNYPPLGNVHLLGYSLGAHAAGIAGSLTNK----KVN 181

QY 181 IIGLDPAGPYFHRSDCPDRLCVTDAYVQVIHT-----SIILGVYNNVGSVDIFYVNYGK 234

Db 182 ITGLDPAGPNFEYAEAPSRSLSPDDADFVDVLTFTRGSPGRSIGIQKPVGHVDIYPNGGT 241

QY 235 NQPGCN-----EPSCSHTKAVKYLTECIKHECCLIGTPMKYFSTPK 276

Db 242 FQPGCNIGELALRVIAERGLGDVDQLVKCSHERSVHLFIDSLNE---ENPSKAYRCNSK 297

QY 277 PISQ-----CRGDTVCVGLNAKSYPAR--GAFYAPVEANAPY 312

Db 298 EAFKGLCLSCRKNRCNNMGYEINKVRAKRSSKMYLKTQRSQMPY 341

RESULT 15

A27330

lipoprotein lipase (EC 3.1.1.34) precursor - guinea pig

C/Species: Cavia porcellus (guinea pig)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C/Accession: JS0398; A27330

R/Enerbaeck, S.; Bjursell, G.

Gene 84, 391-397, 1989

A/Title: Genomic organization of the region encoding guinea pig lipoprotein lipase; evi

A/Reference number: JS0398; MUID:90128283; PMID:2612912

A/Accession: JS0398

A/Molecule type: DNA

A/Residues: 1-465 <EN2>

A/Cross-references: UNIPROT:P1153; GB:M33381; NID:g191268; PIDN:AAA37039.1; PID:g55384

R/Enerback, S.; Semb, H.; Bengtsson-Olivecrona, G.; Carlsson, P.; Hermanson, M.L.; Oli-

Gene 58, 1-12, 1987

A/Title: Molecular cloning and sequence analysis of cDNA encoding lipoprotein lipase of

A/Reference number: A27330; MUID:88084436; PMID:3692172

A/Accession: A27330

A/Molecule type: mRNA

A/Residues: 1-465 <EN2>

A/Cross-references: GB:M15483; NID:g191285; PIDN:AAA37046.1; PID:g305339

C/Genetics: A/Introns: 21/2; 73/3; 133/3; 171/1; 249/1; 330/1; 370/2; 431/2

C/Superfamily: triacylglycerol lipase

C/Keywords: carboxylic ester hydrolase; glycoprotein; heparin binding

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-465/Product: lipoprotein lipase #status experimental <MPT>

F;309-317/Region: heparin binding #status predicted

F;60,376/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;149,173,258/Active site: Ser, Asp, His #status predicted

F;149/Active site: Ser #status predicted

Query Match 17.6%; Score 302.5; DB 1; Length 465;

Best Local Similarity 29.9%; Pred. No. 7.5e-17;

Matches 85; Conservative 37; Mismatches 111; Indels 51; Gaps 9;

QY 63 SKQVFLIHGFLSTGNNEFVAMSKALIEK--DDFLVISVDWKKGACNAFASTKDALGYS 120

Db 62 SSKTFVVIHGWTVTGMYESWPKLVAAALYKREPDNSNVIVDWLSRAQOHYPESAD---YT 118

QY 121 KAVGNTFRHVGEFVADFTKLVEKYYKVLISNIRLIGHSLGAHTSGFAGKEVOKLKGKYE 180
Db 119 KLVGED-----VARFINMEDEFEKYSVDNVHLIGYSLGAHAAGVAGSRTNT---KVS 168
QY 181 IIGDPAGPYFHRSDCPDRLCVTDAEYVQVIHT-----SILGVYNNVGSVDIFYNNYK 234
Db 169 ITGIDPAGPNFEYAEATSRLSPDDAQFVDVLTHTFTRGSPGRSIGIQKPVGHVDIYPNGS 228
QY 235 NQPGCNEP-----SCSHTKAVKYLTECIKHECCLIGTPWKYFSTPK 276
Db 229 FQPGCNIQDALRVISQKGFQDMQVLKCSHERSIHLFIDSLNE----ENPSKAYRCNSK 284
QY 277 PISQ-----CRGDTVCVCGLNAKSYPAR--GAFYAPVEANAPY 312
Db 285 EAFEGICLSCRKRCNNVGYEINKVRAKRSSKMYLKTROMPY 328

Search completed: April 27, 2005, 12:54:36
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 27, 2005, 12:35:36 ; Search time 176 Seconds
(without alignments)
931.053 Million cell updates/sec

Title: US-10-688-011-2

Perfect score: 1721

Sequence: 1 ICFLLDDSTFRNGTLNRGM.....AFYAPVEANAPYCHNEGIKL 320

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1619	94.1	301	1 PA1_POLAN	Q9U6W0 polistes an
2	1444	83.9	337	2 Q6Q252	Q6q252 polistes do
3	1442	83.8	316	2 Q6Q250	Q6q250 polistes do
4	1437	83.5	316	2 Q6Q249	Q6q249 polistes do
5	1437	83.5	316	2 Q6Q251	Q6q251 polistes do
6	949.5	55.2	303	1 PA12_DOLMA	P53357 dolichovesp
7	873.5	50.8	336	1 PA1_VESVU	P49369 vespula vul
8	866	50.3	317	1 PA1_VESVU	Q06478 dolichovesp
9	864	50.2	300	1 PA1_VESMC	P51528 vespula mac
10	357.5	20.8	472	2 Q6P221	Q6p221 xenopus tro
11	357.5	20.8	472	2 Q642T5	Q642t5 xenopus tro
12	353.5	20.5	346	2 Q68KK0	Q68kk0 solenopsis
13	347.5	20.2	460	2 Q6PA23	Q6pa23 xenopus lae
14	345	20.0	576	2 Q7QEY5	Q7qey5 anopheles g
15	342.5	19.9	676	2 Q9VB94	Q9vb94 drosophila
16	340.5	19.8	852	2 Q7PZ17	Q7pz17 anopheles g
17	340	19.8	347	2 Q66KX1	Q66kx1 xenopus lae
18	339	19.7	347	2 Q7SZ70	Q7sz70 xenopus lae
19	339	19.7	481	2 Q6XZB0	Q6xzb0 homo sapien
20	338.5	19.7	472	2 Q642R3	Q642r3 xenopus lae
21	336	19.5	434	2 P81139	P81139 cavia porce
22	333.5	19.4	428	2 Q7Q2S9	Q7q2s9 anopheles g
23	329	19.1	284	2 Q7ZYK0	Q7zyk0 xenopus lae
24	327	19.0	452	2 Q9BDJ4	Q9bdj4 oryctolagus
25	325.5	18.9	481	2 Q6P6S8	Q6p6s8 rattus norv
26	323.5	18.8	540	2 Q9W448	Q9w448 drosophila
27	322	18.7	451	2 Q8WWY8	Q8wwy8 homo sapien
28	322	18.7	525	2 Q7QEY4	Q7qey4 anopheles g
29	321.5	18.7	451	2 Q8CIV3	Q8civ3 mus musculu
30	318.5	18.5	450	1 LIPP_PIG	P00591 sus scrofa
31	316.5	18.4	277	2 Q7QA39	Q7qa39 anopheles g

32	315.5	18.3	449	2 Q8BXB5	Q8bxb5 mus musculu
33	314.5	18.3	456	2 Q6NYZ4	Q6nyz4 brachydanio
34	314.5	18.3	465	2 Q6P8U6	Q6p8u6 mus musculu
35	313.5	18.2	305	2 Q7PZ15	Q7pz15 anopheles g
36	312.5	18.2	461	1 LIPP_HORSE	P29183 equus cabal
37	311.5	18.1	339	2 Q9VB90	Q9vb90 drosophila
38	311.5	18.1	354	2 Q6UW82	Q6uw82 homo sapien
39	311.5	18.1	390	2 Q6ZUS9	Q6zus9 homo sapien
40	310.5	18.0	460	2 Q641F6	Q641f6 xenopus lae
41	310.5	18.0	500	1 LIPE_HUMAN	O9y5x9 homo sapien
42	310.5	18.0	500	2 Q6P9C8	Q6p9c8 homo sapien
43	310.5	18.0	1000	2 Q9VX01	Q9vx01 drosophila
44	310	18.0	341	2 Q9VB88	Q9vb88 drosophila
45	309.5	18.0	475	1 LIPL_MUSVI	O46647 mustela vis

ALIGNMENTS

RESULT 1	PA1_POLAN	STANDARD;	PRT;	301 AA.
AC	Q9U6W0;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Phospholipase A1 (EC 3.1.1.32) (EC 3.1.1.4) (Allergen Pol a 1).			
OS	Polistes annularis (Paper wasp).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;			
OC	Vespidae; Polistinae; Polistes.			
OK	NCBI_TaxID=27505;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	King T.P., Lu G.;			
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Hydrolysis of phosphatidylcholine with phospholipase A2 (EC 3.1.1.4) and phospholipase A1 (EC 3.1.1.32) activities (By similarity).			
CC	-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a carboxylate.			
CC	-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 2-acylglycerophosphocholine + a carboxylate.			
CC	-!- SUBUNIT: Monomer.			
CC	-!- ALLERGEN: Causes an allergic reaction in human.			
CC	-!- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase family.			
CC				
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CC				
DR	EMBL; AF174527; AAD52615.1; -.			
DR	HSSP; P16233; 1GPL.			
DR	InterPro; IPR002334; Dol/Ves_allerg.			
DR	InterPro; IPR000734; Lipase.			
DR	InterPro; IPR008262; Lipase_AS.			
DR	InterPro; IPR000379; Ser_estrs.			
DR	Pfam; PF00151; Lipase; 1.			
DR	PRINTS; PR00821; TAGLIPASE.			
DR	PROSITE; PS00120; LIPASE_SER; 1.			
KW	Allergen; Hydrolase; Lipid degradation.			
FT	ACT_SITE 138 138 Charge relay system (By similarity).			
FT	ACT_SITE 166 166 Charge relay system (By similarity).			
SQ	SEQUENCE 301 AA; 33483 MW; 6A0B7DC76FDC047 CRC64;			
Query Match	94.1%;	Score 1619;	DB 1;	Length 301;
Best Local Similarity	100.0%;	Pred. No. 7.7e-125;		
Matches 301;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 20 MSPDCTFNEKDIVFYVYSRDKRDGIIILKKEITLNYDLFTKSTISKOVFLIHGFLSTGNN 79
Db 1 MSPDCTFNEKDIVFYVYSRDKRDGIIILKKEITLNYDLFTKSTISKOVFLIHGFLSTGNN 60
QY 80 ENFVAMSKALIEKDDFLVISVDMWKGACNAFASTKDALGYSKAVGNTRHVGFVADFTKL 139
Db 61 ENFVAMSKALIEKDDFLVISVDMWKGACNAFASTKDALGYSKAVGNTRHVGFVADFTKL 120
QY 140 LVEKYYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKEIIGLDPAGPYFHRSDCPDR 199
Db 121 LVEKYYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKEIIGLDPAGPYFHRSDCPDR 180
QY 200 LCVTDAEYVQVIHTSIILGVYVNVGSVDFFVYVNGKNQPGCNEPSCSHTKAVKYLTECICKH 259
Db 181 LCVTDAEYVQVIHTSIILGVYVNVGSVDFFVYVNGKNQPGCNEPSCSHTKAVKYLTECICKH 240
QY 260 ECCLIGTPWKKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEGIGK 319
Db 241 ECCLIGTPWKKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEGIGK 300
QY 320 L 320
Db 301 L 301

RESULT 2

Q6Q252

ID Q6Q252 PRELIMINARY; PRT; 337 AA.
AC Q6Q252;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Venom phospholipase A1 precursor.
OS Polistes dominulus (European paper wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Polistes.
OX NCBI_TaxID=34728;
RN [1]

RP SEQUENCE FROM N.A.

RA Moawad T.I.S., Hoffman D.R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY566645; AAS67041.1; -
DR GO; GO:0003824; F:catalytic activity; IEA.

DR GO; GO:0008970; F:phospholipase A1 activity; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.

DR InterPro; IPR002334; DoI/Ves_allerg.
DR InterPro; IPR000734; Lipase.

DR InterPro; IPR008262; Lipase_AS.
DR InterPro; IPR000379; Ser_estrs.

DR Pfam; PF00151; Lipase; 1.
DR PRINTS; PR00825; DOLALLERGEN.

DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KM Signal.

FT SIGNAL 1 21 Potential.
FT CHAIN 36 337 venom phospholipase A1 1.

FT SEQUENCE 337 AA; 37559 MW; C0A7E0E5EBDE448C CRC64;
SQ

Query Match 83.9%; Score 1444; DB 2; Length 337;

Best Local Similarity 83.1%; Pred. No. 2.1e-110;

Matches 265; Conservative 24; Mismatches 30; Indels 0; Gaps 0;

QY 2 CFLDSTFRNGTLNRGMSPDCTFNEKDIVFYVYSRDKRDGIIILKKEITLNYDLFTKST 61
Db 19 CYADDLTLRNGTLDRGITPDCTFNEKDIELHYSRDKRNGIILKKEILKNYDLFOKSQ 78

QY 62 ISQVFLIHGFLSTGNNENFVAMSKALIEKDDFLVISVDMWKGACNAFASTKDALGYSK 121
Db 79 ISHQIALIHGFLSTGNNENFDAMAKALIEIDNFLVISVDMWKGACNAFASTNDVLGYSQ 138

QY 122 AVGNTRHVGFVADFTKLVEKYYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKEI 181
Db 306 VEANAPYCHNEGIGL 320

Db 139 AVGNTRHVGFVADFTKLVEQYKVPMSNIRLIGHSLGAHTSGFAGKEVQRLKGKYKEI 198
QY 182 IGLDPAGPYFHRSDCPDRLCVTDAEYVQVIHTSIILGVYVNVGSVDFFVYVNGKNQPGCNE 241
Db 199 IGLDPAGPSFLTNNKCPNRLCETDAEYVQAIHTSAITLGYYVNVGSVDFFVYVNGKSQPGCSE 258
QY 242 PSCSHTKAVKYLTECIRKHECCLTGTPWKKYFSTPKPISQCRGDTVCVGLNAKSYPARGA 301
Db 259 PSCSHTKAVKYLTECIRKHECCLTGTPWKSYSTPKPISQCRDTCVCGLNAOSYPAGKS 318
QY 302 FYAPVEANAPYCHNEGIGL 320
Db 319 FYVPVDKADAPYCHNEGIGL 337

RESULT 3

Q6Q250

ID Q6Q250 PRELIMINARY; PRT; 316 AA.
AC Q6Q250;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Venom phospholipase A1 3 (Fragment).
OS Polistes dominulus (European paper wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Polistes.
OX NCBI_TaxID=34728;
RN [1]

RP SEQUENCE FROM N.A.

RA Moawad T.I.S., Hoffman D.R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY566647; AAS67043.1; -
DR GO; GO:0003824; F:catalytic activity; IEA.

DR GO; GO:0008970; F:phospholipase A1 activity; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.

DR InterPro; IPR002334; DoI/Ves_allerg.
DR InterPro; IPR000734; Lipase.

DR InterPro; IPR008262; Lipase_AS.
DR InterPro; IPR000379; Ser_estrs.

DR Pfam; PF00151; Lipase; 1.
DR PRINTS; PR00825; DOLALLERGEN.

DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
FT NON_TER 1 1

FT CHAIN 14 >316 venom phospholipase A1 3.
FT NON_TER 316 316

FT SEQUENCE 316 AA; 35019 MW; 12CB3A7748F8FE05 CRC64;
SQ

Query Match 83.8%; Score 1442; DB 2; Length 316;

Best Local Similarity 84.4%; Pred. No. 2.9e-110;

Matches 266; Conservative 21; Mismatches 28; Indels 0; Gaps 0;

QY 6 DDSTFRNGTLNRGMSPDCTFNEKDIVFYVYSRDKRDGIIILKKEITLNYDLFTKSTISKQ 65
Db 2 DDLTLRNGTLDRGITPDCTFNEKDIELHYSRDKRNGIILKKEILKNYDLFOKSQISHQ 61

QY 66 VVFLIHGFLSTGNNENFVAMSKALIEKDDFLVISVDMWKGACNAFASTKDALGYSKAVGN 125
Db 62 IAILIHGFLSTGNNENFDAMAKALIEIDNFLVISVDMWKGACNAFASTNDVLGYSQAVGN 121

QY 126 TRHVGFVADFTKLVEKYYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKGKYKEIIGLD 185
Db 122 TRHVGFVADFTKLVEQYKVPMSNIRLIGHSLGAHTSGFAGKEVQRLKGKYKEIIGLD 181

QY 186 PAGPYFHRSDCPDRLCVTDAEYVQVIHTSIILGVYVNVGSVDFFVYVNGKNQPGCNEPSCS 245
Db 182 PAGPSFLTSCPDRLCETDAEYVQAIHTSAITLGYYVNVGSVDFFVYVNGKSQPGCSEPCS 241

QY 246 HTKAVKYLTECIRKHECCLTGTPWKKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAP 305
Db 242 HTKAVKYLTECIRKHECCLTGTPWKSYSTPKPISQCRDTCVCGLNAOSYPAGKSFYVP 301

QY 306 VEANAPYCHNEGIGL 320

RA	Hoffman D.R.;
RT	"Allergens in hymenoptera venom. XXVI: the complete amino acid sequences of two vespid venom phospholipases.";
RL	Int. Arch. Allergy Immunol. 104:184-190(1994).
CC	-1- FUNCTION: Hydrolysis of phosphatidylcholine with phospholipase A2 (EC 3.1.1.4) and phospholipase A1 (EC 3.1.1.32) activities.
CC	-1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC	acylglycerophosphocholine + a carboxylate.
CC	-1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 2-
CC	acylglycerophosphocholine + a carboxylate.
CC	-1- ALLERGEN: Causes an allergic reaction in human.
CC	-1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase family.
DR	PIR; A44563; A44563.
DR	HSSP; P54318; 1BU8.
DR	InterPro; IPR002334; Dol/Ves_allerg.
DR	InterPro; IPR000734; Lipase.
DR	InterPro; IPR008262; Lipase_AS.
DR	InterPro; IPR000379; Ser_estrs.
DR	Pfam; PF00151; Lipase; 1.
DR	PRINTS; PR00821; TAGLIPASE.
KW	PROSITE; PS00120; LIPASE_SER; 1.
KM	Allergen; Direct protein sequencing; Hydrolase; Lipid degradation; Multigene family.
FT	ACT_SITE 140 140 Charge relay system (By similarity).
FT	ACT_SITE 168 168 Charge relay system (By similarity).
FT	VARIANT 55 55 G -> E.
FT	VARIANT 295 295 F -> Y.
SO	SEQUENCE 303 AA; 33782 MW; 85816A837C0F3AF8 CRC64;

Query Match	55.2%;	Score 949.5;	DB 1;	Length 303;
Best Local Similarity	57.6%;	Pred. No. 8.4e-70;		
Matches 175; Conservative	52;	Mismatches 68;	Indels 9;	Gaps 5;

Qy		19	GMSPDCTFNEKDIVEFYVYSRDKRDGIIILKKELTNTNYDLFTKSTI-SKÖVFLIHGFISTG	77
Dd		1	GILPECKLVBEISFVLSTRENRDGVYTLÖKLKNKMFXNSDLSKKVPFLIHGFISSA	60
Qy		78	NNENFVAMSKALIEKDDFLVISVDWKKGAC-NAFASTKDALGYSAVENTRHVGKFVADF	136
Dd		61	TNKNYADMTRALLLDKDDIMVISIDWRDGCASNEFALLK-FIGYPKAVENTRAVGKYIADF	119
Qy		137	TKLIVEXKYKYLISNIRLIGHSLGAHTSGPAGKEVÖKLTGLKXKEIIGLDPRAGPYEHRSDC	196
Dd		120	SKILIÖKYKYLLENIRRLIGHSLGAÖLAGFAKGEFÖRFKLGTKYPEIIGLDPAGPSFKKKDC	179
Qy		197	PDRLCVTDAEVÖVIHTSIIIGVYYNVGSVDFFVNYGXNQPGCN--EPSCSHTKAVKYL	253
Dd		180	PERICETDAHYÖILHTSSNLGTERTLGTVDFYINDGSNQPGCTYIIIGETCSHTRAVKYL	239
Qy		254	TECIKHCECLIGTPWKXYFSTPKPIISOGRGDTCVCVGLNAKSYPARGAFYAPVEANAPYC	313
Dd		240	TECIRRECCLIGVPÖSK--NPÖPVSKCTRNECVCGLNAXEPKKGSFYVPVEAKADFC	296
Qy		314	HNEG 317	
Dd		297	NNNG 300	

```

RESULT 7
PAL_VESVU
ID PAL_VESVU STANDARD; PRT; 336 AA.
AC P49369;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Phospholipase A1 precursor (EC 3.1.1.32) (Allergen Ves v
DE 1) (Ves v I).
OS Vesputia vulgaris (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vesputia.
OX NCBI TaxID=7454;

```

RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 37-65; 165-183; 247-263 AND
 RP 273-294.
 RX MEDLINE=96426243; PubMed=8828537;
 RA King T.P., Lu G., Gonzalez M., Qian N., Soldatova L.;
 RT "Yellow jacket venom allergens, hyaluronidase and phospholipase:
 RT sequence similarity and antigenic cross-reactivity with their hornet
 RT and wasp homologs and possible implications for clinical allergy.";
 RL J. Allergy Clin. Immunol. 98:588-600(1996).
 CC -1- FUNCTION: Hydrolysis of phosphatidylcholine with phospholipase A2
 CC (EC 3.1.1.4) and phospholipase A1 (EC 3.1.1.32) activities (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a carboxylate.
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 2-
 CC acylglycerophosphocholine + a carboxylate.
 CC -1- ALLERGEN: Causes an allergic reaction in human.
 CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
 CC family.
 CC -----
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	DR	Intra; IPR009786; Ser_1.	Dbl/Ves_allerg.
	DR	InterPro; IPR002334;	Lipase_AS.
	DR	InterPro; IPR000734;	Lipase_AS.
	DR	InterPro; IPR008262;	Ser_estrs.
	DR	Pfam; PF00151;	LIPASE_SER; 1.
	DR	PROSITE; PS00120;	LIPASE_SER; 1.
KW	Allergen;	Direct protein sequencing;	Hydrolase; Lipid degradation;
KW	Signal.		
FT	SIGNAL	1	36
FT	CHAIN	37	336
FT	ACT_SITE	173	173
FT	ACT_SITE	201	201
FT	CONFLICT	37	37
SO	SEQUENCE	336 AA;	37676 MW; 65548B7F5DBE56456 CRC64;

Query Match	50.8%;	Score 873.5;	DB 1;	Length 336;
Best Local Similarity	52.0%;	Pred. No. 1.7e-63;		
Matches 166;	Conservative 55;	Mismatches 87;	Indels 11;	Gaps 4;

[illegible]

```
RESULT 8
PAL_DOLMA STANDARD; PRT; 317 AA.
AC Q06478;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Phospholipase A1 precursor (EC 3.1.1.32) (EC 3.1.1.4) (Allergen Dol
DE m 1.01) (Dol m 1) (Fragment).
OS Dolichovespula maculata (White-face hornet) (Bald-faced hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Dolichovespula.
OX NCBI_TaxID=7441;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=93209375; PubMed=8458431; DOI=10.1016/0014-5793(93)80080-E;
RA Soldatova L., Kochoumian L., King T.P.;
RT "Sequence similarity of a hornet (D. maculata) venom allergen
RT phospholipase A1 with mammalian lipases.";
RL FEBS Lett. 320:145-149(1993).
CC -1- FUNCTION: Hydrolysis of phosphatidylcholine with phospholipase A2
CC (EC 3.1.1.4) and phospholipase A1 (EC 3.1.1.32) activities.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 2-
CC acylglycerophosphocholine + a carboxylate.
CC -1- ALLERGEN: Causes an allergic reaction in human.
CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X66869; CAA47341.1; -.
DR PIR; S32406; S32406.
DR HSSP; P54318; 1BU8.
DR InterPro; IPR002334; Dol/Ves_allerg.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR008262; Lipase_AS.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00151; Lipase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Allergen; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Lipid degradation; Multigene family; Signal.
FT NON_TER 1
FT SIGNAL <1 17
FT CHAIN 18 317 Phospholipase A1 1.
FT ACT_SITE 154 154 Charge relay system (By similarity).
FT ACT_SITE 182 182 Charge relay system (By similarity).
FT CARBOHYD 25 25 N-linked (GlcNAc. . .).
FT CARBOHYD 229 229 N-linked (GlcNAc. . .) (Potential).
FT VARIANT 271 271 N -> S.
SQ SEQUENCE 317 AA; 35708 MW; 0B2135FD453512D9 CRC64;

Query Match 50.3%; Score 866; DB 1; Length 317;
Best Local Similarity 54.5%; Pred. No. 6.5e-63;
Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2;

QY 24 CTFNEKDIVVYVSRDKRGGIILKKEITLNYDLFTKSTISQOVFLIHGFLSTGNNEFV 83
Db 21 CPFSNDTVKMIFLTRENKRKHDFYTLDTMNRHNEFKKSIKRPFVFTTHGFTSSATEKNFV 80
QY 84 AMSKALIEKDFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGKFAVADFTKLLVEK 143
Db 81 AMSKALMHTGDFLIIMVDWRMAACTDDEYPLGLKYMFKAAVGNTRLVGNFIAMIAKLVEQ 140
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QY 144 YKVLISNIRLIGSLGAHTSGFAGKEVQKLKGKYKEIIGDPAGPFYHRSDCPRLCVT 203
Db 141 YKVPMTNIRLVGHSLSGAHISGFAGKYQELKGFSEIIGDPAGPSFKNDCSERICET 200
QY 204 DAEVVOVHTSIIIGVYVNVGSVDVYVNYGKNQPGCN---EPSCSHTKAVKYLTECIKHE 260
Db 201 DAHYVQIILHTSSNLGTERLTGTVDFYINNNGSNQPGCRYITIGETCSHTRAVKYFTECI RRE 260
QY 261 CCLIGTPWKKYFTSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317
Db 261 CCLIGVPOSK--NPQPVSKCTRNCEVCVGLNAKKYPKRGSFYVPEAEAPYCNNG 314

RESULT 9
PAL_VESMC STANDARD; PRT; 300 AA.
AC P51528;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Phospholipase A1 (EC 3.1.1.32) (EC 3.1.1.4) (Allergen Ves m 1) (Ves m
DE 1).
OS Vespula maculifrons (Eastern yellow jacket) (Waap).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=7453;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94257972; PubMed=8199462;
RA Hoffman D.R.;
RT "Allergens in hymenoptera venom. XXVI: the complete amino acid
RT sequences of two vespid venom phospholipases.";
RL Int. Arch. Allergy Immunol. 104:184-190(1994).
CC -1- FUNCTION: Hydrolysis of phosphatidylcholine with phospholipase A2
CC (EC 3.1.1.4) and phospholipase A1 (EC 3.1.1.32) activities (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 2-
CC acylglycerophosphocholine + a carboxylate.
CC -1- SUBUNIT: Monomer.
CC -1- ALLERGEN: Causes an allergic reaction in human.
CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC family.
DR PIR; A44564; A44564.
DR HSSP; P00591; 1ETH.
DR InterPro; IPR002334; Dol/Ves_allerg.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR008262; Lipase_AS.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00151; Lipase; 1.
DR PRINTS; PR00821; TAGLIPASE.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Allergen; Direct protein sequencing; Hydrolase; Lipid degradation.
FT ACT_SITE 137 137 Charge relay system (By similarity).
FT ACT_SITE 165 165 Charge relay system (By similarity).
FT VARIANT 97 97 A -> M.
FT VARIANT 191 191 I -> P.
FT VARIANT 202 202 I -> L.
SQ SEQUENCE 300 AA; 33540 MW; 8EE2DE20BD69CGF6 CRC64;

Query Match 50.2%; Score 864; DB 1; Length 300;
Best Local Similarity 54.0%; Pred. No. 8.9e-63;
Matches 162; Conservative 51; Mismatches 79; Indels 8; Gaps 4;

QY 22 PDCTFNEKDIVVYVSRDKRGGIILKKEITLNYDLFTKSTISQOVFLIHGFLSTGNNEF 81
Db 2 PKCPFSNDTVSIIETRENRRDLTYLTQLQNHPEFKKKTITRPVFTTHGFTSSASEKN 61
QY 82 FVAMSKALIEKDFLVISVDWKKGAC-NAFASTKDALGYSKAVGNTRHVGKFAVADFTKLL 140
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Db      62 FINLAKALVDKDNMYVISIDWQTAACNTNEYPGLKAY-YPTAASNTRLVGQYIATITOKL 120
QY      141 VEKYKVLISNIRLIGSLGAHTSGFAGKEVQKLKLGKYKEIIGLDPAGPYFHRSDCPDRL 200
Db      121 VKDYKISMANIRLIGSLGAHVGSGFAGKRVQELKLGKYSIIIGLDPARPSFDSNHCSERL 180
QY      201 CVTDAEYVQVIHTSIILGVYVNGSVDFYVNYGKNQPCGN--EPSCSHTXAVKYLTECI 257
Db      181 CETDAEYVQIHTSNYLTGTEKILGTVDYFMNNGKNPCGRFSEVCSHTRAVIYMAECI 240
QY      258 KHECCLTGTPWKYFSTPKPISQCRGDTCCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317
Db      241 KHECCLTGTPRSK---SSQPSRCTKQECVCVGLNAKCYPSRGSFYVPVESTAPFCNNKG 297

RESULT 10
06P2Z1
ID      Q6P2Z1      PRELIMINARY;      PRT;      472 AA.
AC      Q6P2Z1;
DT      05-JUL-2004 (TREMBLrel. 27, Created)
DT      05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE      Hypothetical protein MGC76224.
GN      Name=MGC76224;
OS      Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8364;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RA      Klein S., Gerhard D.S.;
RL      Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC      -!- SIMILARITY: Contains 1 PLAT domain.
DR      EMBL; BC064243; AAH64243.1; -.
DR      GO; GO:0003824; F:catalytic activity; IEA.
DR      GO; GO:0004806; F:triacylglycerol lipase activity; IEA.
DR      GO; GO:0006629; P:lipid metabolism; IEA.
DR      InterPro; IPR000734; Lipase.
DR      InterPro; IPR008262; Lipase_AS.
DR      InterPro; IPR002331; Lipase_panc.
DR      InterPro; IPR001024; Lipoxxygenase_LH2.
DR      InterPro; IPR008976; PLAT_LH2.
DR      InterPro; IPR000379; Ser_estrs.
DR      Pfam; PF00151; Lipase; 1.
DR      Pfam; PF01477; PLAT; 1.
DR      PRINTS; PR00823; PANCLIPASE.
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DR      PRINTS; PRO0821; TAGLIPASE.
DR      SMART; SM00308; LH2; 1.
DR      PROSITE; PS00120; LIPASE_SER; 1.
KW      Hypothetical protein.
SQ      SEQUENCE 472 AA; 51948 MW; 3B5407A2BA9A6D6 CRC64;

Query Match      20.8%; Score 357.5; DB 2; Length 472;
Best local Similarity 31.0%; Pred. No. 6.5e-21;
Matches 91; Conservative 43; Mismatches 109; Indels 51; Gaps 7;

QY      50 TLINYDLFTKSTISKQVFLIHGFLSTGNNEFVAMSKALIEKDFLISVDWKGCACNA 109
Db      79 SLTNFKTSRKS-----FIHGFIDEGEENLVNCKAMLKVEDVNCFTDMSGSRIT 132
QY      110 FASTKDALGYSKAVGNTRHVGKFNADFTKLVEKYKVLISNIRLIGSLGAHTSGFAGKE 169
Db      133 -----YTQAAANNIRVVGAEALAYFIGYLSKMKYPPLSNVHIIGSLGSHTAGEVGKR 183
QY      170 VQKLKLGKYKEIIGLDPAGPYFHRSDCPDRLCVTDAEYVQVIHT-----SIILGVYIN 222
Db      184 MPGI-----GRITGLDPAGPYFQNTPIEVRLDPTDAVFDAIHTDPLIPKMGYMSQS 238
QY      223 VGSVDYVYNYGKNQPCNEP-----SCSHTXAVKYLTECIKHECCL 263
Db      239 VAHMDFFPENGGENMPGSKPIIAKLIDIGMEGSKDIFACNHLRSYKYTESSSPDGF 298
QY      264 IGTPEWKYFSTPKPIS-QCRGDTCCVGLNAKSYPARG---AFYAPVEANAPY 312
Db      299 VGYPSTSYEAFTKGTGTFCTTCGCPLMGHYADAFSSHGTSDSYSFLNTGSEKPY 352
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RESULT 11
0642T5
ID      Q642T5      PRELIMINARY;      PRT;      472 AA.
AC      Q642T5;
DT      25-OCT-2004 (TREMBLrel. 28, Created)
DT      25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE      Hypothetical protein.
OS      Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8364;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RA      Klein S., Gerhard D.S.;
RL      Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
```


RA Williams S.M., Woodager T, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[2]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutcon G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
RN
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
RN
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
[7]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003758; AAF56648.1; -;
DR EMBL; AY118607; AAM49976.1; -;
DR HSSP; PS4318; 1BU8.
DR FlyBase; FBgn0039470; CG6296.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008970; F:phospholipase A1 activity; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR002334; D01/Ves_allerg.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00151; Lipase; 1.
DR PRINTS; PR00825; DOLALLERGEN.
DR PRINTS; PR00821; TAGLIPASE.
SQ SEQUENCE 676 AA; 72427 MW; 6A707E13C7AC5CCC CRC64;

Query Match		19.9%	Score 342.5;	DB 2;	Length 676;
Best Local Similarity		30.1%	Pred. No.1.7e-19;		
Matches		93;	Conservative 41;	Mismatches 106;	Indels 69; Gaps 10;
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QY	80 ENFVAMSKALLIEKDFLVISVDWKKGACNAFASTKALGYSKAVGNTRHVGKFAVDFTKL 139				
Db	119 GVNTRVADAWFOYGDYNMIAVDWLGR-----SLEYASSVAGAPGAGKVAALVDF 169				
QY	140 LVEKYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKLGKYKEIIGLDPAGPYFHRSDCPDR 199				
Db	170 LVEGYGMSLDLTLEIVGFSLGAHVAGHTAKQVNSGKVGK---VGLDPASPLISYSNTEKR 226				
QY	200 LCVTDAEYVQVIHTS-IILGVYVNVGSVDFFYVNVYGNQBPQCN---EPSCSHTKAVKYLTE 255				
Db	227 LSSD DALYVESIQTN GAILGFQPIGKASFYMNGGRSGPGCGIDITGSCSHTKAVLYVE 286				
QY	256 CIKHECCLICTPWKKYFSTPKPISQCR-----GDT--CVCVGLNAKSYFARGAFY 303				
Db	287 ALL-----WNNF-----PSIKCESSVDANKNNGNTYSSVFMGASINFEVAEGIFY 332				
QY	304 APVEANAPY 312				
Db	333 VPVNKESPY 341				

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Job time : 179 secs

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